GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 10, 2003, 17:54:40 ; Search time 361 Seconds
(without alignments)
9132.758 Million cell updates/sec

Title: US-09-787-962-1_COPY_1046_2509
Perfect score: 1464
Sequence: 1 atggatgctaatggaggacc.....cggttaagatcgatctttga 1464

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1464	100.0	1464	21	AAC42778	Arabidopsis thalia
2	1464	100.0	2509	22	AAF62693	Arabidopsis KCS2 g
3	1133	77.4	1704	16	AAQ90217	Condensing enzyme
4	903.4	61.7	1853	21	AAC50224	Arabidopsis thalia
5	901.2	61.6	1611	20	AAX23221	A. thaliana EL5 DN
6	889.8	60.8	1855	21	AAC37776	Arabidopsis thalia
7	725	49.5	1548	20	AAX23223	A. thaliana EL7 DN
8	706.2	48.2	1819	21	AAC39559	Arabidopsis thalia
9	652.4	44.6	1641	17	AAT27036	Arabidopsis fatty
10	652.4	44.6	1709	24	AAD28500	Arabidopsis thalia
11	652.4	44.6	1792	21	AAZ35524	Fatty acid elongas
12	650.8	44.5	1709	24	AAD28517	Arabidopsis thalia
13	647.6	44.2	1521	24	AAD28513	Brassica napus elo
14	641.2	43.8	1521	24	AAD28514	A. thaliana FAE1-B
15	641.2	43.8	1521	24	AAD28537	Alternative versio
16	637.6	43.6	1664	16	AAQ90218	Condensing enzyme
17	628.4	42.9	1521	24	AAD28518	A. thaliana FAE1-B
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19	620.4	42.4	1521	24	AAD28520	B. napus elongase
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24	616.8	42.1	1521	24	AAD28535	Alternative versio
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33	610.8	41.7	1524	24	AAD28516	Brassica napus fat
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36	609.2	41.6	1524	24	AAD28501	Brassica napus fat
37	599.4	40.9	1512	20	AAX23219	A. thaliana EL3 DN
38	598.6	40.9	1479	20	AAX23218	A. thaliana EL2 DN
39	595.6	40.7	1588	22	AAF62738	Plant FAE1 gene 5'
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42	585.4	40.0	607	16	AAQ90214	Arabadopsis conden
43	580	39.6	2143	22	AAH50968	Ketoacyl ACP synth
44	578.8	39.5	1442	16	AAQ90212	Brassica Reston va
45	575.6	39.3	1442	16	AAQ90211	Brassica condensin

ALIGNMENTS

RESULT 1
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AC AAC42778;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36814.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
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XX
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XX
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XX
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RESULT 2
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ID   AAF62693 standard; DNA; 2509 BP.
XX
AC   AAF62693;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Arabidopsis KCS2 genomic DNA.
XX
KW   Long chain fatty acid condensing enzyme; KCS2;
KW   beta-ketoacyl-coenzyme A synthase 2; cosuppression; antisense;
KW   screening; ds.
XX
OS   Arabidopsis sp.
XX
```

PN WO200107586-A2.
XX
PD 01-FEB-2001.
XX
PF 21-JUL-2000; 2000WO-CA00860.
XX
PR 22-JUL-1999; 99US-0145013.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Kunst L, Clemens S;
XX
DR WPI; 2001-168548/17.
XX
PT Novel nucleic acid sequence encoding plant long chain fatty acid (LCFA)
PT condensing enzyme (fatty acid elongase) useful for producing transgenic
PT plants having altered fatty acid content in the tissues
XX
PS Example 1; Fig 1; 32pp; English.
XX
[redacted] The present invention relates to a plant long chain fatty acid
condensing enzyme, KCS2 (beta-ketoacyl-coenzyme A synthase 2).
CC The invention is useful in cosuppression or antisense inhibition,
CC as a plant breeding tool, as molecular markers to aid in plant
CC breeding programs and in screening
XX
SQ Sequence 2509 BP; 748 A; 478 C; 497 G; 786 T; 0 other;

Query Match 100.0%; Score 1464; DB 22; Length 2509;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGATGCTAATGGAGGACCTGTACAGATCCGGACCCAAAACTACGTCAAGCTTGGTTAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 ATGGATGCTAATGGAGGACCTGTACAGATCCGGACCCAAAACTACGTCAAGCTTGGTTAT 1105

Qy         61 CACTATCTGATCACTCACTTTTTTAAACTCATGTTCCTCCCTCTAATGGCTGTTTTGTTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 ATGAATGTCTCATTGTTAAGCCTAAACCATCTTCAGCTCTATTACAATTCCACCGGATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 ATGAATGTCTCATTGTTAAGCCTAAACCATCTTCAGCTCTATTACAATTCCACCGGATTC 1225

Qy        181 ATCTTCGTCATTACTCTCGCCATTGTCGGATCCATTGTCTTCTTCATGTCTCGACCTAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1226 ATCTTCGTCATTACTCTCGCCATTGTCGGATCCATTGTCTTCTTCATGTCTCGACCTAGA 1285

Qy        241 TCCATCTACCTTCTAGATTACTCTTGCTACCTCCCGCCTTCGAGTCAAAAAGTTAGCTAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 TCCATCTACCTTCTAGATTACTCTTGCTACCTCCCGCCTTCGAGTCAAAAAGTTAGCTAC 1345

Qy        301 CAGAAATTCATGAACAACTCTAGTTTGATTCAAGATTTCAGCGAAACTTCTCTTGAGTTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1346 CAGAAATTCATGAACAACTCTAGTTTGATTCAAGATTTCAGCGAAACTTCTCTTGAGTTC 1405

Qy        361 CAGAGGAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTATT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1406 CAGAGGAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTATT 1465

Qy        421 CACTCTATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAATC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1466 CACTCTATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAATC 1525

Qy        481 TTCGGTGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTGTT 540
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Db       1526 TTCGGTGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTGTT 1585

Qy        541 CTTGTTGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTAAC 600
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Db       1586 CTTGTTGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTAAC 1645

Qy        601 AAGTATAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTGCT 660
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Db       1646 AAGTATAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTGCT 1705

Qy        661 GGTGTTATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTGCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1706 GGTGTTATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTGCT 1765

Qy        721 CTTGTGGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAATG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1766 CTTGTGGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAATG 1825

Qy        781 TTGATCCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGCCT 840
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Db       1826 TTGATCCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGCCT 1885

Qy        841 TTGGATCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGATCT 900
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Db       1886 TTGGATCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGATCT 1945

Qy        901 GATGAGAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1946 GATGAGAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAGTT 2005

Qy        961 TCTTTGTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTTCT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2006 TCTTTGTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTTCT 2065

Qy       1021 TTGGGTCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTGCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2066 TTGGGTCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTGCT 2125

Qy       1081 AAGAGATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTTTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2126 AAGAGATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTTTA 2185

Qy       1141 GATCATTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTTTA 1200
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Db       2186 GATCATTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTTTA 2245

Qy       1201 AAGCTTTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACACT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2246 AAGCTTTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACACT 2305

Qy       1261 TCCTCTAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2306 TCCTCTAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGAAA 2365

Qy       1321 GGAAACAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTTGG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2366 GGAAACAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTTGG 2425

Qy       1381 GTGGCTCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATAGA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2426 GTGGCTCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATAGA 2485

Qy       1441 TATCCGGTTAAGATCGATCTTTGA 1464
              ||||||||||||||||||||||||
Db       2486 TATCCGGTTAAGATCGATCTTTGA 2509
```

RESULT 3
AAQ90217
ID AAQ90217 standard; cDNA; 1704 BP.
XX
AC AAQ90217;
XX
DT 04-DEC-1995 (first entry)
XX
DE Condensing enzyme clone Lunaria 1.
XX
KW Lunaria; condensing enzyme; ss.
XX
OS Lunaria annua.

```
XX
FH   Key             Location/Qualifiers
FT   CDS             42..1538
FT                   /*tag= a
FT   misc_feature    345
FT                   /*tag= b
FT                   /note= "unspecified nt"
XX
PN   WO9515387-A.
XX
PD   08-JUN-1995.
XX
PF   30-NOV-1994;   94WO-US13686.
XX
PR   23-JUN-1994;   94US-0265047.
PR   30-NOV-1993;   93US-0160602.
XX
PA   (CALJ ) CALGENE INC.
XX
PI   Lardizabal KD,  Lassner MW,  Metz JG;
XX
DR   WPI; 1995-215267/28.
DR   P-PSDB; AAR77171.
XX
PT   Production of very long chain fatty acid(s) in plant(s) - to produce
PT   drought and stress resistant transgenic plant(s)
XX
PS   Claim 9; Figure 12; 149pp; English.
XX
CC   The CE15 and CE20 Brassica cDNA sequences (see AAQ90210,Q90211
CC   and AAQ90212) and the condensing enzyme encoding sequence from
CC   jojoba (AAQ90208) were used in determining primers AAQ90221-
CC   AAQ90225 from conserved AAs. These primers were variously used to
CC   PCR (RTPCR) amplify fragments from RNA isolated from developing
CC   seeds of Lunaria annua, Tropaoelu majus (Nasturtium), and
CC   green liliques of Arabidopsis thaliana. The primers most
CC   successfully utilised were AAQ90221 and AAQ90222. These primers were
CC   used to produce three clones encoding a portion of the elongase
CC   condensing enzyme from Arabidopsis. From Lunaria a single clone
CC   was identified, LUN CE8. A cDNA library from RNA isolated from
CC   developing seeds of Lunaria was constructed, and LUN CE8 was used
CC   to screen this library. Three classes of cDNA clones were isolated,
CC   Lunaria 1, Lunaria 5 and Lunaria 27. Lunaria 5 shares approx.
CC   85% homology with the Brassica CE20 clones, and it is suggested
CC   that it is active in seed oik fatty acid elongation.
XX
SQ   Sequence 1704 BP; 474 A; 359 C; 381 G; 489 T; 1 other;

  Query Match             77.4%;  Score 1133;  DB 16;  Length 1704;
  Best Local Similarity   86.5%;  Pred. No. 0;
  Matches 1282;  Conservative    0;  Mismatches  176;  Indels   24;  Gaps    2;

Qy          7 GCTAATGGAGGACCTGTACAGATCCGGACCCAAAACTACGTCAAGCTTGGTTATCACTAT 66
Db         57 GTTAATGGAGGATCCGTACAGATCCGGACCCGAAAGTACGTCAAGCTGGGTTATCACTAC 116

Qy         67 CTGATCACTCACTTTTTAAACTCATGTTCCTCCCTCTAATGGCTGTTTTGTTCATGAAT 126
Db        117 CTGATTTCTCACCTTTTAAGCTCTTGTTGGTTCCTTTAATGGCGGTTCTGTTCACGAAT 176

Qy        127 GTCTCATTGTTAAGCCTAAACCA------------------TCTTCAGCTCTATTACAAT 168
Db        177 GTCTCCCGGTTAAGCCTAAACCAGCTCTGTCTCGATCTCTCTCTCCAGCTCCAGTTCAAT 236

Qy        169 TCCACCGGATTCATCTTCGTCATTACTCTCGCCATTGTCGGATCCATTGTCTTCTTCATG 228
Db        237 CTCGTCGGATTCATCTTCTTCATTACCGCCTCCATTTTCGGATTCACAGTTATCTTCATG 296

Qy        229 TCTCGACCTAGATCCATCTACCTTCTAGATTACTCTTGCTACCTCCCGCCTTCGAGTCAA 288
Db        297 TCCCGACCTAGATCCGTTTACCTCCTCGACTACTCATGTTACCTCCCGNCGGCGAATCTC 356

Qy        289 AAAGTTAGCTACCAGAAATTCATGAACAACTCTAGTTTGATTCAAGATTTCAGCGAAACT 348
Db        357 AAAGTTAGCTACCAGACATTCATGAATCATTCTAAACTGATTGAAGATTTCGACGAGTCG 416

Qy        349 TCTCTTGAGTTCCAGAGGAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTA 408
Db        417 TCGCTTGAGTTCCAGCGGAAGATCCTGAAGCGATCCGGTCTCGGCGAAGAGACTTACCTC 476

Qy        409 CCGGATTCTATTCACTCTATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCG 468
Db        477 CCGGAATCTATCCACTGCATCCCGCCGCGTCCGACTATGGCGGCGGCGCGTGAGGAATCG 536

Qy        469 GAGCAGGTAATCTTCGGTGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGG 528
Db        537 GAGCAGGTAATCTTCGGTGCACTCGACAATCTCTTCGAGAATACCAAAATCGACCCTAGG 596

Qy        529 GAGATTGGTGTTCTTGTTGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCC 588
Db        597 GAGATTGGTGTTGTGGTGGTGAACTGCAGCTTGTTTAACCCGACGCCTTCTTTATCCGCC 656

Qy        589 ATGATTGTTAACAAGTATAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATG 648
Db        657 ATGATTGTGAACAAGTATAAGCTTAGAGGAAACGTGAAGAGCTTTAACCTCGGAGGAATG 716

Qy        649 GGATGTAGTGCTGGTGTTATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGG 708
Db        717 GGATGTAGGGCTGGTGTCATCGCCCGTTGATCTCGCTAATGACATTTTACAGCTCCATAGA 776

Qy        709 AACACTTTTGCTCTTGTGGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAAC 768
Db        777 AACACATTAGCTCTTGTGGTTAGCACAGAGAACATCACTCAGAATTGGTACTTTGGTAAC 836

Qy        769 AAGAAAGCAATGTTGATCCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTT 828
Db        837 AACAAAGCAATGTTGATTCCTAATTGCTTGTTTAGGGTTGGTGGATCCGCGGTTCTGCTT 896

Qy        829 TCGAACAAGCCTTTGGATCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACT 888
Db        897 TCGAACAAGCCTCGTGATCGAAAACGATCCAAGTATAAACTTGTTCACACGGTACGGACT 956

Qy        889 CATAAAGGATCTGATGAGAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTG 948
Db        957 CATAAAGGATCTGATGAGAAAGCATTCAACTGTGTGTACCAAGAACAAGACGAGGACTTG 1016

Qy        949 AAAACCGGAGTTTCTTTGTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACG 1008
Db       1017 AAAACCGGAGTTTCTTTGTCTAAAGACCTAATGTCTATAGCTGGAGAAGCTCTAAAGACA 1076

Qy       1009 AATATCACTTCTTTGGGTCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCG 1068
Db       1077 AATATCACCACTTTGGGTCCTCTGGTTCTTCCAATAAGCGAGCAGATTCTGTTCATTGCG 1136

Qy       1069 ACTTTTGTTGCTAAGAGATTGTTCAATG------ACAAGAAGAAGAAGCCTTACATACCG 1122
Db       1137 ACTTTTGTTCCAAAGAGATTGTTCAGTGCCAAGAAGAAGAAGAAGAAGCCTTACATACCG 1196

Qy       1123 GATTTCAAGCTTGCTTTAGATCATTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGAT 1182
Db       1197 GATTTCAAGCTTGCCTTTGATCATTTCTGTATTCACGCAGGAGGTAGAGCCGTGATCGAT 1256

Qy       1183 GAGCTAGAGAAGAGTTTAAAGCTTTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTG 1242
Db       1257 GAACTAGAGAAGAGTTTAAAGCTATTGCCAAAACATGTGGAGGCTTCTAGAATGACATTG 1316

Qy       1243 CATAGATTTGGAAACACTTCCTCTAGCTCTATATGGTATGAATTGGCTTACACGGAAGCT 1302
Db       1317 CATAGATTTGGAAACACTTCATCGAGCTCTATTTGGTATGAATTAGCTTACACAGAAGCT 1376

Qy       1303 AAAGGAAGAATGAGGAAAGGAAACAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAG 1362
Db       1377 AAAGGAAGAATGAGAAAAGGGAATCGAGTTTGGCAGATTGCTTTTGGAAGCGGCTTTAAG 1436

Qy       1363 TGTAACAGCGCGGTTTGGGTGGCTCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGG 1422
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Db       1437 TGTAACAGCGCGGTTTGGGTGGCTCTTCGTGATGTCGAGCCCTCGGTTAACAATCCTTGG 1496

Qy       1423 GAACATTGCATCCATAGATATCCGGTTAAGATCGATCTTTGA 1464
              |||||||||||||||||||||||||||||||||||| |||
Db       1497 GAACATTGCATCCATAGATATCCGGTTAAGATCGATCTCTGA 1538


RESULT 4
AAC50224
ID   AAC50224 standard; DNA; 1853 BP.
XX
AC   AAC50224;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 64036.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
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PR   04-MAY-1999;   99US-0132484.
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PR   17-JUN-1999;   99US-0139492.
PR   18-JUN-1999;   99US-0139454.
PR   18-JUN-1999;   99US-0139455.
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PR   18-JUN-1999;   99US-0139462.
PR   18-JUN-1999;   99US-0139463.
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PR   12-JUL-1999;   99US-0142977.
PR   13-JUL-1999;   99US-0143542.
PR   14-JUL-1999;   99US-0143624.
PR   15-JUL-1999;   99US-0144005.
PR   16-JUL-1999;   99US-0144085.
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PR   20-JUL-1999;   99US-0144884.
PR   21-JUL-1999;   99US-0144814.
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PR   23-JUL-1999;   99US-0145218.
PR   23-JUL-1999;   99US-0145224.
PR   26-JUL-1999;   99US-0145276.
PR   27-JUL-1999;   99US-0145913.
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PR   27-JUL-1999;   99US-0145919.
PR   28-JUL-1999;   99US-0145951.
PR   02-AUG-1999;   99US-0146386.
PR   02-AUG-1999;   99US-0146388.
PR   02-AUG-1999;   99US-0146389.
PR   03-AUG-1999;   99US-0147038.
PR   04-AUG-1999;   99US-0147204.
PR   04-AUG-1999;   99US-0147302.
PR   05-AUG-1999;   99US-0147192.
PR   05-AUG-1999;   99US-0147260.
PR   06-AUG-1999;   99US-0147303.
PR   06-AUG-1999;   99US-0147416.
PR   09-AUG-1999;   99US-0147493.
PR   09-AUG-1999;   99US-0147935.
PR   10-AUG-1999;   99US-0148171.
PR   11-AUG-1999;   99US-0148319.
PR   12-AUG-1999;   99US-0148341.
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PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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PR 16-SEP-1999; 99US-0154039.
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PR 22-SEP-1999; 99US-0155139.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 61.7%; Score 903.4; DB 21; Length 1853;
Best Local Similarity 77.4%; Pred. No. 1.1e-251;
Matches 1128; Conservative 0; Mismatches 311; Indels 18; Gaps 2;

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Qy         23 TACAGATCCGGACCCAAAACTACGTCAAGCTTGGTTATCACTATCTGATCACTCACTTTT 82
              |||| | |   | |   || |||||||||||| |||||||| || || || |||||  | |
Db        252 TACAAAGCGTCAACATGAAATACGTCAAGCTAGGTTATCATTACCTCATTACTCATCTCT 311

Qy         83 TTAAACTCATGTTCCTCCCTCTAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAGCC 142
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Db        312 TCAAGCTCTGTTTGGTTCCATTAATGGCGGTTTTAGTCACAGAGATCTCTCGATTAACAA 371

Qy        143 TAAACCAT--------------CTTCAGCTCTATTACAATTCCACCGGATTCATCTTCG 187
                | || ||              ||||| ||| | |||||| |   |  ||||||||
Db        372 CAGACGATCTTTACCAGATTTGGCTTCATCTCCAATACAATCTCGTTGCTTTCATCTTTC 431

Qy        188 TCATTACTCTCGCCATTGTCGGATCCATTGTCTTCTTCATGTCTCGACCTAGATCCATCT 247
              ||  | || | || ||  | || |||| || | | ||||  ||| || |||||  | |
Db        432 TCTCTGCTTTAGCTATCTTTGGCTCCACCGTTTACATCATGAGTCGTCCCAGATCTGTTT 491

Qy        248 ACCTTCTAGATTACTCTTGCTACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAAAT 307
              | ||  | |||||||||||| || || || ||   |||||   | ||||  || ||||| |
Db        492 ATCTCGTTGATTACTCTTGTTATCTTCCTCCGGAGAGTCTTCAGGTTAAGTATCAGAAGT 551

Qy        308 TCATGAACAACTCTAGTTTGATTCAAGATTTCAGCGAAACTTCTCTTGAGTTCCAGAGGA 367
              | ||| |  | ||||  |||||| |||||||||  ||  | ||| | ||||| |||||||
Db        552 TTATGGATCATTCTAAGTTGATTGAAGATTTCAATGAGTCATCTTTAGAGTTTCAGAGGA 611

Qy        368 AGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTATTCACTCTA 427
              ||||  |    || |||||| | || ||||||||||| | || ||  || | || | ||
Db        612 AGATTCTTGAACGTTCTGGTTTAGGAGAAGAGACTTATCTCCCTGAAGCTTTACATTGTA 671

Qy        428 TCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAATCTTCGGTG 487
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Db        672 TCCCTCCGAGGCCTACGATGATGGCGGCTCGTGAGGAATCTGAGCAGGTAATGTTTGGTG 731

Qy        488 CACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTGTTCTTGTTG 547
              | || || || |||||||||||||| || || || |||||||| ||||||||  | ||||
Db        732 CTCTTGATAAGCTTTTCGAGAATACCAAGATTAACCCTAGGGATATTGGTGTGTTGGTTG 791

Qy        548 TGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTAACAAGTATA 607
              |||||||||| |||||||| ||||| ||||| || || || ||||||||||||||||||
Db        792 TGAATTGTAGCTTGTTTAATCCTACACCTTCGTTGTCAGCTATGATTGTTAACAAGTATA 851

Qy        608 AGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTGCTGGTGTTA 667
              |||||||||| ||  ||||||| |||||||||| |||||||| ||||||||||||||||
Db        852 AGCTTAGAGGGAATGTTAAGAGTTTTAACCTTGGTGGAATGGGGTGTAGTGCTGGTGTTA 911

Qy        668 TCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTGCTCTTGTGG 727
              || |  | ||| |||||  |||||||| ||| | |||||||| |||| |||| ||||||
Db        912 TCTCTATCGATTTAGCTAAAGATATGTTGCAAGTTCATAGGAATACTTATGCTGTTGTGG 971

Qy        728 TTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAATGTTGATCC 787
              |||||||||||||||| |||||||||||||||||||| || ||||| || |||||||| |
Db        972 TTAGTACTGAGAACATTACTCAGAATTGGTATTTTGGGAATAAGAAGGCTATGTTGATTC 1031

Qy        788 CTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGCCTTTGGATC 847
              | ||||| |||||| | |||||||||||| ||| || || | |||||||||      ||||
Db       1032 CGAATTGTTTGTTTCGTGTTGGTGGTTCGGCGATTTTGTTGTCGAACAAGGGGAAAGATC 1091

Qy        848 GAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGATCTGATGAGA 907
              | | ||| || |||||||||||||||||||| || ||||||||||||||| ||| |||||
Db       1092 GTAGACGGTCTAAGTATAAGCTTGTTCATACCGTTAGGACTCATAAAGGAGCTGTTGAGA 1151

Qy        908 ACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAGTTTCTTTGT 967
              | || ||||| ||||| || ||||| ||||||||   |  ||| |||||  ||||| ||||
Db       1152 AGGCTTTCAACTGTGTTTACCAAGAGCAAGATGATAATGGGAAGACCGGGGTTTCGTTGT 1211

Qy        968 CTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTTCTTTGGGTC 1027
              | |||||||||||||||||||||| |||||| | ||| |||||||||| |||| ||||
Db       1212 CGAAAGATCTTATGGCTATAGCTGGGGAAGCTCTTAAGGCGAATATCACTACTTTAGGTC 1271

Qy       1028 CTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTGCTAAGAGAT 1087
              || ||||||||||||||| ||||||||||||||  ||   |||||| ||| | |||| |
Db       1272 CTTTGGTTCTTCCTATAAGTGAGCAGATTCTGTTTTTCATGACTTTGGTTACGAAGAAAC 1331

Qy       1088 TGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTTTAGATCATT 1147
              ||||  | ||  |||| |||||| || || |||||||||||||||| || |||||||
Db       1332 TGTT---TAACTCGAAGCTGAAGCCGTATATTCCGGATTTCAAGCTTGCGTTTGATCATT 1388

Qy       1148 TCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTTTAAAGCTTT 1207
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Db       1389 TCTGTATCCATGCTGGTGGTAGAGCTGTGATTGATGAGCTTGAGAAGAATCTGCAGCTTT 1448

Qy       1208 CTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACACTTCCTCTA 1267

Db       1449 CGCAGACTCATGTCGAGGCATCCAGAATGACACTGCACAGATTTGGAAACACTTCTTCGA 1508

Qy       1268 GCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGAAAGGAAACA 1327

Db       1509 GCTCGATTTGGTATGAACTGGCTTACATAGAGGCTAAAGGTAGGATGAAGAAAGGAAACC 1568

Qy       1328 GAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTTGGGTGGCTC 1387

Db       1569 GGGTTTGGCAGATTGCTTTTGGAAGTGGGTTTAAGTGTAACAGTGCAGTTTGGGTGGCTC 1628

Qy       1388 TTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATAGATATCCGG 1447

Db       1629 TAAACAATGTCAAGCCTTCGGTTAGTAGTCCGTGGGAACACTGCATCGACCGATATCCGG 1688

Qy       1448 TTAAGATCGATCTTTGA 1464

         1689 TTAAGCTCGACTTCTGA 1705
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RESULT 5
AAX23221
ID   AAX23221 standard; DNA; 1611 BP.
XX
AC   AAX23221;
XX
DT   11-JUN-1999  (first entry)
XX
DE   A. thaliana EL5 DNA.
XX
KW   EL5; very long chain fatty acid; VLCFA; beta-keto acyl synthase;
KW   plant; vegetable oil; lubricant; fuel; feedstock; plastic; cosmetic;
KW   pharmaceutical; edible oil; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   WO9854954-A1.
XX
PD   10-DEC-1998.
XX
PF   01-JUN-1998;   98WO-US11384.
XX
PR   03-JUN-1997;   97US-0868373.
XX
PA   (CRGI ) CARGILL INC.
PA   (JAWO/) JAWORSKI J G.
PA   (POST/) POST-BEITTENMILLER MA.
PA   (TODD/) TODD J.
XX
PI   Jaworski JG,  Post-Beittenmiller MA,  Todd J;
XX
DR   WPI; 1999-070227/06.
DR   P-PSDB; AAW93431.
XX
PT   New isolated beta-keto acyl synthase polynucleotides - used
PT   particularly for the production of transgenic plants having altered
PT   levels of very long chain fatty acids in tissues
XX
PS   Claim 9; Fig 11; 76pp; English.
XX
CC   This invention describes the isolation of beta-keto acyl synthase
CC   proteins from Arabidopsis thaliana. The products of the invention
CC   can be used for producing vegetable oils having elevated levels of
CC   very long chain fatty acids (VLCFA) for use as e.g. lubricants, fuels
CC   and as a feedstock for plastics, pharmaceuticals and cosmetics. The
CC   products can also be used for producing oils having reduced levels of
CC   VLCFAs for use as edible oils. This sequence encodes EL5.
XX
SQ   Sequence 1611 BP; 413 A; 288 C; 382 G; 528 T; 0 other;
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  Query Match           61.6%;  Score 901.2;  DB 20;  Length 1611;
  Best Local Similarity  77.5%;  Pred. No. 4.3e-251;
  Matches 1124;  Conservative    0;  Mismatches  308;  Indels   18;  Gaps    2;

Qy         23 TACAGATCCGGACCCAAAACTACGTCAAGCTTGGTTATCACTATCTGATCACTCACTTTT 82

Db        161 TACAAAGCGTCAACATGAAATACGTCAAGCTAGGTTATCATTACCTCATTACTCATCTCT 220

Qy         83 TTAAACTCATGTTCCTCCCTCTAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAGCC 142

Db        221 TCAAGCTCTGTTTGGTTCCATTAATGGCGGTTTTAGTCACAGAGATCTCTCGATTAACAA 280

Qy        143 TAAACCAT----------CTTCAGCTCTATTACAATTCCACCGGATTCATCTTCG 187

Db        281 CAGACGATCTTTACCAGATTTGGCTTCATCTCCAATACAATCTCGTTGCTTTCATCTTTC 340

Qy        188 TCATTACTCTCGCCATTGTCGGATCCATTGTCTTCTTCATGTCTCGACCTAGATCCATCT 247

Db        341 TCTCTGCTTTAGCTATCTTTGGCTCCACCGTTTACATCATGAGTCGTCCCAGATCTGTTT 400

Qy        248 ACCTTCTAGATTACTCTTGCTACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAAAT 307

Db        401 ATCTCGTTGATTACTCTTGTTATCTTCCTCCGGAGAGTCTTCAGGTTAAGTATCAGAAGT 460

Qy        308 TCATGAACAACTCTAGTTTGATTCAAGATTTCAGCGAAACTTCTCTTGAGTTCCAGAGGA 367

Db        461 TTATGGATCATTCTAAGTTGATTGAAGATTTCAATGAGTCATCTTTAGAGTTTCAGAGGA 520

Qy        368 AGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTATTCACTCTA 427

Db        521 AGATTCTTGAACGTTCTGGTTTAGGAGAAGAGACTTATCTCCCTGAAGCTTTACATTGTA 580

Qy        428 TCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAATCTTCGGTG 487

Db        581 TCCCTCCGAGGCCTACGATGATGGCGGCTCGTGAGGAATCTGAGCAGGTAATGTTTGGTG 640

Qy        488 CACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTGTTCTTGTTG 547

Db        641 CTCTTGATAAGCTTTTCGAGAATACCAAGATTAACCCTAGGGATATTGGTGTGTTGGTTG 700

Qy        548 TGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTAACAAGTATA 607

Db        701 TGAATTGTAGCTTGTTTAATCCTACACCTTCGTTGTCAGCTATGATTGTTAACAAGTATA 760

Qy        608 AGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTGCTGGTGTTA 667

Db        761 AGCTTAGAGGGAATGTTAAGAGTTTTAACCTTGGTGGAATGGGGTGTAGTGCTGGTGTTA 820

Qy        668 TCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTGCTCTTGTGG 727

Db        821 TCTCTATCGATTTAGCTAAAGATATGTTGCAAGTTCATAGGAATACTTATGCTGTTGTGG 880

Qy        728 TTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAATGTTGATCC 787

Db        881 TTAGTACTGAGAACATTACTCAGAATTGGTATTTTGGGAATAAGAAGGCTATGTTGATTC 940

Qy        788 CTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGCCTTTGGATC 847

Db        941 CGAATTGTTTGTTTCGTGTTGGTGGTTCGGCGATTTTGTTGTCGAACAAGGGGAAAGATC 1000

Qy        848 GAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGATCTGATGAGA 907

Db       1001 GTAGACGGTCTAAGTATAAGCTTGTTCATACCGTTAGGACTCATAAAGGAGCTGTTGAGA 1060

Qy        908 ACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAGTTTCTTTGT 967

Db       1061 AGGCTTTCAACTGTGTTTACCAAGAGCAAGATGATAATGGGAAGACCGGGGTTTCGTTGT 1120

Qy        968 CTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTTCTTTGGGTC 1027

Db       1121 CGAAAGATCTTATGGCTATAGCTGGGGAAGCTCTTAAGGCGAATATCACTACTTTAGGTC 1180

Qy       1028 CTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTGCTAAGAGAT 1087
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Db       1181 CTTTGGTTCTTCCTATAAGTGAGCAGATTCTGTTTTTCATGACTTTGGTTACGAAGAAAC 1240

Qy       1088 TGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTTTAGATCATT 1147

Db       1241 TGTT---TAACTCGAAGCTGAAGCCGTATATTCCGGATTTCAAGCTTGCGTTTGATCATT 1297

Qy       1148 TCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTTTAAAGCTTT 1207

Db       1298 TCTGTATCCATGCTGGTGGTAGAGCTGTGATTGATGAGCTTGAGAAGAATCTGCAGCTTT 1357

Qy       1208 CTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACACTTCCTCTA 1267

Db       1358 CGCAGACTCATGTCGAGGCATCCAGAATGACACTGCACAGATTTGGAAACACTTCTTCGA 1417

Qy       1268 GCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGAAAGGAAACA 1327

Db       1418 GCTCGATTTGGTATGAACTGGCTTACATAGAGGCTAAAGGTAGGATGAAGAAAGGAAACC 1477

Qy       1328 GAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTTGGGTGGCTC 1387

Db       1478 GGGTTTGGCAGATTGCTTTTGGAAGTGGGTTTAAGTGTAACAGTGCAGTTTGGGTGGCTC 1537

Qy       1388 TTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATAGATATCCGG 1447

Db       1538 TAAACAATGTCAAGCCTTCGGTTAGTAGTCCGTGGGAACACTGCATCGACCGATATCCGG 1597

Qy       1448 TTAAGATCGA 1457

Db       1598 TTAAGCTCGA 1607
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RESULT 6
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ID AAC37776 standard; DNA; 1855 BP.
XX
AC AAC37776;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18626.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 60.8%; Score 889.8; DB 21; Length 1855;
Best Local Similarity 77.3%; Pred. No. 9.4e-248;
Matches 1126; Conservative 0; Mismatches 312; Indels 19; Gaps 3;

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Qy      23 TACAGATCCGGACCCAAAACTACGTCAAGCTTGGTTATCACTATCTGATCACTCACTTTT 82
           |||| | |   | |   || ||||||||||| |||||||| || || || ||||| | |
Db     254 TACAAAGCGTCAACATGAAATACGTCAAGCTAGGTTATCATTACCTCATTACTCATCTCT 313

Qy      83 TTAAACTCATGTTCCTCCCTCTAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAGCC 142
           | || ||| || | ||  ||||||| ||||| ||| |  ||| ||||
Db     314 TCAAGCTCTGTTTGGTTCCATTAATGGCGGTTTTAGTCACAGAGACCTCTCGATTAACAA 373

Qy     143 TAAACCAT--------------CTTCAGCTCTATTACAATTCCACCGGATTCATCTTCG 187
           | || ||                ||||| ||| | ||||||  |   | ||||||||
Db     374 CAGACGATCTTTACCAGATTTGGCTTCATCTCCAATACAATCTCGTTGCTTTCATCTTTC 433

Qy     188 TCATTACTCTCGCCATTGTCGGATCCATTGTCTTCTTCATGTCTCGACCTAGATCCATCT 247
           ||  | || | || ||  | || ||||  || | | ||||| ||| || |||||  | |
Db     434 TCTCTGCTTTAGCTATCTTTGGCTCCACCGTTTACATCATGAGTCGTCCCAGATCTGTTT 493

Qy     248 ACCTTCTAGATTACTCTTGCTACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAAAT 307
           | ||  | ||||||||||| || || || ||   |||||   | ||||  || ||||| |
Db     494 ATCTCGTTGATTACTCTTGTTATCTTCCTCCGGAGAGTCTTCAGGTTAAGTATCAGAAGT 553

Qy     308 TCATGAACAACTCTAGTTTGATTCAAGATTTCAGCGAAACTTCTCTTGAGTTCCAGAGGA 367
           | ||| |  | ||||  |||||| |||||||||  ||  | ||| | ||||| |||||||
Db     554 TTATGGATCATTCTAAGTTGATTGAAGATTTCAATGAGTCATCTTTAGAGTTTCAGAGGA 613

Qy     368 AGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTATTCACTCTA 427
           ||||  |    || |||||| | || |||||||||||| | || ||  || | || | ||
Db     614 AGATTCTTGAACGTTCTGGTTTAGGAGAAGAGACTTATCTCCCTGAAGCTTTACATTGTA 673

Qy     428 TCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAATCTTCGGTG 487
           |||||||| | ||||| |||   || || ||||| ||| | ||||||||||| || ||||
Db     674 TCCCTCCGAGGCCTACGATGATGGCGGCTCGTGAGGAATCTGAGCAGGTAATGTTTGGTG 733

Qy     488 CACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTGTTCTTGTTG 547
           | || || || |||||||||||||| || || || |||||||| ||||||||  | ||||
Db     734 CTCTTGATAAGCTTTTCGAGAATACCAAGATTAACCCTAGGGATATTGGTGTGTTGGTTG 793

Qy     548 TGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTAACAAGTATA 607
           |||||||||| |||||||| ||||| ||||| || || || ||||||||||||||||||||
Db     794 TGAATTGTAGCTTGTTTAATCCTACACCTTCGTTGTCAGCTATGATTGTTAACAAGTATA 853

Qy     608 AGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTGCTGGTGTTA 667
           |||||||||| ||  ||||||| |||||||||| |||||||| ||||||||||||||||||
Db     854 AGCTTAGAGGGAATGTTAAGAGTTTTAACCTTGGTGGAATGGGGTGTAGTGCTGGTGTTA 913

Qy     668 TCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTGCTCTTGTGG 727
           || |  | ||| ||||||  |||||||| ||| | |||||||| |||| |||| ||||||
Db     914 TCTCTATCGATTTAGCTAAAGATATGTTGCAAGTTCATAGGAATACTTATGCTGTTGTGG 973

Qy     728 TTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAATGTTGATCC 787
           |||||||||||||||| |||||||||||||||||||| || ||||| || |||||||| |
Db     974 TTAGTACTGAGAACATTACTCAGAATTGGTATTTTGGGAATAAGAAGGCTATGTTGATTC 1033

Qy     788 CTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGCCTTTGGATC 847
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Db       1034 CGAATTGTTTGTTTCGTGTTGGTGGTTCGGCGATTTTGTTGTCGAACAAGGGGAAAGATC 1093

Qy        848 GAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGATCTGATGAGA 907

Db       1094 GTAGACGGTCTAAGTATAAGCTTGTTCATACCGTTAGGACTCATAAAGGAGCTGTTGAGA 1153

Qy        908 ACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAGTTTCTTTGT 967

Db       1154 AGGCTTTCAACTGTGTTTACCAAGAGCAAGATGATAATGGGAAGACCGGGGTTTCGTTGT 1213

Qy        968 CTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTTCTTTGGGTC 1027

Db       1214 CGAAAGATCTTATGGCTATAGCTGGGGAAGCTCTTAAGGCGAATATCACTACTTTAGGTC 1273

Qy       1028 CTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTGCTAAGAGAT 1087

Db       1274 CTTTGGTTCTTCCTATAAGTGAGCAGATTCTGTTTTTCATGACTTTGGTTACGAAGAAAC 1333

Qy       1088 TGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTTTAGATCATT 1147

Db       1334 TGTT---TAACTCGAAGCTGAAGCCGTATATTCCGAATTTCAAGCTTGCGTTTGATCATT 1390

Qy       1148 TCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTTTAAAGCTTT 1207

Db       1391 TCTGTATCCATGCTGGTGGTAGAGCTGTGATTGATGAGCTTGAGAAGAATCTGCAGCTTT 1450

Qy       1208 CTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACACTTCCTCTA 1267

Db       1451 CGCAGACTCATGTCGAGGCATCGAGAATGACACTGCATAGATTTGGAAACACTTCTTCGA 1510

Qy       1268 GCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGAAAGGAAACA 1327

Db       1511 GCTCGATTTGGTATGAACTGGCTTACATAGAGGCTAAAGGTAGGATGAAGAAAGGAAACC 1570

Qy       1328 GAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTTGGGTGGCTC 1387

Db       1571 GGGTTTGGCAGATTGCTTTTGGAAGTGGGTTTAAGTGTAACAGTGCAGTTTGGGTGGCTC 1630

Qy       1388 TTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATAGATATCCGG 1447

Db       1631 TAAACAATGTCAAG-CTTCGGTTAGTAGTCCGTGGGAACACTGCATCGACCGATATCCGG 1689

Qy       1448 TTAAGATCGATCTTTGA 1464

Db       1690 TTAAGCTCGACTTCTGA 1706
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RESULT 7
AAX23223
ID AAX23223 standard; DNA; 1548 BP.
XX
AC AAX23223;
XX
DT 11-JUN-1999 (first entry)
XX
DE A. thaliana EL7 DNA.
XX
KW EL7; very long chain fatty acid; VLCFA; beta-keto acyl synthase;
KW plant; vegetable oil; lubricant; fuel; feedstock; plastic; cosmetic;
KW pharmaceutical; edible oil; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO9854954-A1.
XX
PD 10-DEC-1998.
XX
PF 01-JUN-1998; 98WO-US11384.
XX
PR 03-JUN-1997; 97US-0868373.
XX
PA (CRGI) CARGILL INC.
PA (JAWO/) JAWORSKI J G.
PA (POST/) POST-BEITTENMILLER MA.
PA (TODD/) TODD J.
XX
PI Jaworski JG, Post-Beittenmiller MA, Todd J;
XX
DR WPI; 1999-070227/06.
DR P-PSDB; AAW93433.
XX
PT New isolated beta-keto acyl synthase polynucleotides - used
PT particularly for the production of transgenic plants having altered
PT levels of very long chain fatty acids in tissues
XX
PS Claim 9; Fig 15; 76pp; English.
XX
CC This invention describes the isolation of beta-keto acyl synthase
CC proteins from Arabidopsis thaliana. The products of the invention
CC can be used for producing vegetable oils having elevated levels of
CC very long chain fatty acids (VLCFA) for use as e.g. lubricants, fuels
CC and as a feedstock for plastics, pharmaceuticals and cosmetics. The
CC products can also be used for producing oils having reduced levels of
CC VLCFAs for use as edible oils. This sequence encodes EL7.
XX
SQ Sequence 1548 BP; 401 A; 303 C; 371 G; 473 T; 0 other;

Query Match 49.5%; Score 725; DB 20; Length 1548;
Best Local Similarity 70.0%; Pred. No. 6.1e-200;
Matches 1012; Conservative 0; Mismatches 415; Indels 18; Gaps 2;

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Qy         21 TGTACAGATCCGGACCCAAAACTACGTCAAGCTTGGTTATCACTATCTGATCACTCACTT 80

Db         96 TCTCCAGAGCGTGAATCTCAAGTATGTGAAATTAGGTTACCATTACTTAATCTCAAATCT 155

Qy         81 TTTTAAACTCATGTTCCTCCCTCTAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAG 140

Db        156 CTTGACTCTCTGTTTATTCCCTCTCGCCGTTGTTATCTCCGTCGAAGCCTCTCAGATGAA 215

Qy        141 CCTAAACCATCTT----------------CAGCTCTATTACAATTCCACCGGATTCATCTT 185

Db        216 CCCAGATGATCTCAAACAGCTCTGGATCCATCTACAATACAATCTGGTTAGTATCATCAT 275

Qy        186 CGTCATTACTCTCGCCATTGTCGGATCCATTGTCTTCTTCATGTCTCGACCTAGATCCAT 245

Db        276 CTGTTCAGCGATTCTAGTCTTCGGGTTAACGGTTTATGTTATGACCCGACCTAGACCCGT 335

Qy        246 CTACCTTCTAGATTACTCTTGCTACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAA 305

Db        336 TTACTTGGTTGATTTCTCTTGTTATCTCCCACCTGATCATCTCAAAGCTCCTTACGCTCG 395

Qy        306 ATTCATGAACAACTCTAGTTTGATTCAAGATTTCAGCGAAACTTCTCTTGAGTTCCAGAG 365

Db        396 GTTCATGGAACATTCTAGACTCACCGGAGATTTCGATGACTCTGCTCTCGAGTTTCAACG 455

Qy        366 GAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTATTCACTC 425

Db        456 CAAGATCCTTGAGCGTTCTGGTTTAGGGGAAGACACTTATGTCCCTGAAGCTATGCATTA 515

Qy        426 TATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAATCTTCGG 485

Db        516 TGTTCCACCGAGAATTTCAATGGCTGCTGCTAGAGAAGAAGCTGAACAAGTCATGTTTGG 575

Qy        486 TGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTGTTCTTGT 545

Db        576 TGCTTTAGATAACCTTTTCGCTAACACTAATGTGAAACCAAAGGATATTGGAATCCTTGT 635

Qy        546 TGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTAACAAGTA 605

Db        636 TGTGAATTGTAGTCTCTTTAATCCAACTCCTTCGTTATCTGCAATGATTGTGAACAAGTA 695

Qy        606 TAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTGCTGGTGT 665

Db        696 TAAGCTTAGAGGTAACATTAGAAGCTACAATCTAGGCGGTATGGGTTGCAGCGCGGGAGT 755
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Qy       666 TATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTGCTCTTGT 725
             |||||| || ||||| |||  || |||||     | ||||||||||||| |||  ||||
Db       756 TATCGCTGTGGATCTTGCTAAAGACATGTTGTTGGTACATAGGAACACTTATGCGGTTGT 815

Qy       726 GGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAATGTTGAT 785
              |||  |||||||||||| |||||||||||||||||||||||||||| | ||||||||
Db       816 TGTTTCTACTGAGAACATTACTCAGAATTGGTATTTTGGTAACAAGAAATCGATGTTGAT 875

Qy       786 CCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGCCTTTGGA 845
             || || |||||||||| |||||||||| || |||||| |||| ||||||||| |   |||
Db       876 ACCGAACTGCTTGTTTCGAGTTGGTGGCTCTGCGGTTTTGCTATCGAACAAGTCGAGGGA 935

Qy       846 TCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGATCTGATGA 905
              | ||| || ||||| | |||||| ||| · ||||||||||     ||| | |||||
Db       936 CAAGAGACGGTCTAAGTACAGGCTTGTACATGTAGTCAGGACTCACCGTGGAGCAGATGA 995

Qy       906 GAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAGTTTCTTT 965
             || || |||  |||||| |||||||| || |||||       || |||||| ||||| ||
Db       996 TAAAGCTTTCCGTTGTGTTTATCAAGAGCAGGATGATACAGGGAGAACCGGGGTTTCGTT 1055

Qy       966 GTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTTCTTTGGG 1025
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Db      1056 GTCGAAAGATCTAATGGCGATTGCAGGGGAAACTCTCAAAACCAATATCACTACATTGGG 1115

Qy      1026 TCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTGCTAAGAG 1085
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Db      1116 TCCTCTTGTTCTACCGATAAGTGAGCAGATTCTCTTCTTTATGACTCTAGTTGTGAAGA- 1174

Qy      1086 ATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTTTAGATCA 1145
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Db      1175 --AGCTCTTTAACGGTAAAGTGAAACCGTATATCCCGGATTTCAAACTTGCTTTCGAGCA 1232

Qy      1146 TTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTTTAAAGCT 1205
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Db      1233 TTTCTGTATCCATGCTGGTGGAAGAGCTGTGATCGATGAGTTAGAGAAGAATCTGCAGCT 1292

Qy      1206 TTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACACTTCCTC 1265
             ||| |||   ||||| ||||| || || |||||| | ||| ||||||| ||||| || ||
Db      1293 TTCACCAGTTCATGTCGAGGCTTCGAGGATGACTCTTCATCGATTTGGTAACACATCTTC 1352

Qy      1266 TAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGAAAGGAAA 1325
              |||||| || |||||||||||||||||||  ||||| || ||||| ||| | | ||| ||
Db      1353 GAGCTCCATTTGGTATGAATTGGCTTACATTGAAGCGAAGGGAAGGATGCGAAGAGGTAA 1412

Qy      1326 CAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTTGGGTGGC 1385
              | |||||||| || || || || || || ||||| ||||| |||||| ||||||  ||
Db      1413 TCGTGTTTGGCAAATCGCGTTCGGAAGTGGATTTAAATGTAATAGCGCGATTTGGGAAGC 1472

Qy      1386 TCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATAGATATCC 1445
              |  |  |||| · | || |||   |||| |||||||||| |||| ||  | |  |||||
Db      1473 ATTAAGGCATGTGAAACCTTCGAACAACAGTCCTTGGGAAGATTGTATTGACAAGTATCC 1532

Qy      1446 GGTTA 1450
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Db      1533 GGTAA 1537
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RESULT 8
AAC39559
ID AAC39559 standard; DNA; 1819 BP.
XX
AC AAC39559;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 25077.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX

PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 48.2%; Score 706.2; DB 21; Length 1819;
Best Local Similarity 69.7%; Pred. No. 1.9e-194;
Matches 1007; Conservative 0; Mismatches 418; Indels 20; Gaps 3;

```
Qy        21 TGTACAGATCCGGACCCAAAACTACGTCAAGCTTGGTTATCACTATCTGATCACTCACTT 80
             | | |||| |  ||  |  || || || ||  | |||||  | ||  | ||| | |  |
Db       231 TCTCCAGAGCGTGAATCTCAAGTATGTGAAATTAGGTTACAATTACTTAATCTCAAATCT 290

Qy        81 TTTTAAACTCATGTTCCTCCCTCTAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAG 140
              || |  |||   ||  |||||||   | |||| | | |  | | |||   | | |
Db       291 CTTGACTCTCTGTTTATTCCCTCTCGCCGTTGTTATCTCCGTCGAAGCCTCTCAGATGAA 350

Qy       141 CCTAAACCATCTT----------CAGCTCTATTACAATTCCACCGGATTCATCTT 185
             || | |  ||||           || ||  | ||||||       |  ||||| |
Db       351 CCCAGATGATCTCAAACAGCTCTGGATCCATCTACAATACAATCTGGTTAGTATCATCAT 410

Qy       186 CGTCATTACTCTCGCCATTGTCGGATCCATTGTCTTCTTCATGTCTCGACCTAGATCCAT 245
             |      |  |     |  |||| |  |  || |   | | | |||||||| || |
Db       411 CTGTTCAGCGATTCTAGTCTTCGGGTTAACGGTTTATGTTACGACCCGACCTAGACCCGT 470

Qy       246 CTACCTTCTAGATTACTCTTGCTACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAA 305
             |||  |  | |||| |||||| || ||||| |||     ||  |||| |   |||
Db       471 TTACTTGGTTGATTTCTCTTGTTATCTCCCACCTGATCATCTCAAAGCTCCTTACGCTCG 530

Qy       306 ATTCATGAACAACTCTAGTTTGATTCAAGATTTCAGCGAAACTTCTCTTGAGTTCCAGAG 365
             ||||||  |  ||||| | |     |||||||   ||   || |||| ||||| ||  |
Db       531 GTTCATGGAACATTCTAGACTCACCGGAGATTTCGATGACTCTGCTCTCGAGTTTCAACG 590

Qy       366 GAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTATTCACTC 425
             ||||||  |    || |||||| | || ||||| |||  | | || ||  |||| || |
Db       591 CAAGATCCTTGAGCGTTCTGGTTTAGGGGAAGACACT--TGTCCCTGAAGCTATGCATTA 648
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Qy       426 TATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAATCTTCGG 485
Db       649 TGTTCCACCGAGAATTTCAATGGCTGCTGCTAGAGAAGAAGCTGAACAAGTCATGTTTGG 708

Qy       486 TGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTGTTCTTGT 545
Db       709 TGCTTTAGATAACCTTTTCGCTAACACTAATGTGAAACCAAAGGATATTGGAATCCTTGT 768

Qy       546 TGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTAACAAGTA 605
Db       769 TGTGAATTGTAGTCTCTTTAATCCAACTCCTTCGTTATCTGCAATGATTGTGAACAAGTA 828

Qy       606 TAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTGCTGGTGT 665
Db       829 TAAGCTTAGAGGTAACATTAGAAGCTACAATCTAGGCGGTATGGGTTGCAGCGCGGGAGT 888

Qy       666 TATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTGCTCTTGT 725
Db       889 TATCGCTGTGGATCTTGCTAAAGACATGTTGTTGGTACATAGGAACACTTATGCGGTTGT 948

Qy       726 GGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAATGTTGAT 785
Db       949 TGTTTCTACTGAGAACATTACTCAGAATTGGTATTTTGGTAACAAGAAATCGATGTTGAT 1008

Qy       786 CCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGCCTTTGGA 845
Db      1009 ACCGAACTGCTTGTTTCGAGTTGGTGGCTCTGCGGTTTTGCTATCGAACAAGTCGAGGGA 1068

Qy       846 TCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGATCTGATGA 905
Db      1069 CAAGAGACGGTCTAAGTACAGGCTTGTACATGTAGTCAGGACTCACCGTGGAGCAGATGA 1128

Qy       906 GAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAGTTTCTTT 965
Db      1129 TAAAGCTTTCCGTTGTGTTTATCAAGAGCAGGATGATACAGGGAGAACCGGGGTTTCGTT 1188

Qy       966 GTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTTCTTTGGG 1025
Db      1189 GTCGAAAGATCTAATGGCGATTGCAGGGGAAACTCTCAAAACCAATATCACTACATTGGG 1248

Qy      1026 TCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTGCTAAGAG 1085
Db      1249 TCCTCTTGTTCTACCGATAAGTGAGCAGATTCTCTTCTTTATGACTCTAGTTGTGAAGA- 1307

Qy      1086 ATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTTTAGATCA 1145
Db      1308 --AGCTCTTTAACGGTAAAGTGAAACCGTATATCCCGGATTTCAAACTTGCTTTCGAGCA 1365

Qy      1146 TTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTTTAAAGCT 1205
Db      1366 TTTCTGTATCCATGCTGGTGGAAGAGCTGTGATCGATGAGTTAGAGAAGAATCTGCAGCT 1425

Qy      1206 TTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACACTTCCTC 1265
Db      1426 TTCACCAGTTCATGTCGAGGCTTCGAGGATGACTCTTCATCGATTTGGTAACACATCTTC 1485

Qy      1266 TAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGAAAGGAAA 1325
Db      1486 GAGCTCCATTTGGTATGAATTGGCTTACATTGAAGCGAAGGGAAGGATGCGAAGAGGTAA 1545

Qy      1326 CAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTTGGGTGGC 1385
Db      1546 TCGTGTTTGGCAAATCGCGTTCGGAAGTGGATTTAAATGTAATAGCGCGATTTGGGAAGC 1605

Qy      1386 TCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATAGATATCC 1445
Db      1606 ATTAAGGCATGTGAAACCTTCGAACAACAGTCCTTGTGAAGATTGTATTGACAAGTATCC 1665

Qy      1446 GGTTA 1450
Db      1666 GGTAA 1670
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RESULT 9
AAT27036
ID AAT27036 standard; cDNA; 1641 BP.
XX
AC AAT27036;
XX
DT 14-OCT-1996 (first entry)
XX
DE Arabidopsis fatty acid elongation gene FAE1 cDNA clone.
XX
KW Fatty acid elongation gene; FAE1; transgenic plant; seed oil;
KW vegetable oil; Brassica napus; canola; oilseed rape;
KW eicosenoic acid; erucic acid; antisense; ss.
XX
OS Arabidopsis thaliana ecotype Ws.
XX
FH Key   Location/Qualifiers
FT CDS   1..1521
FT   /*tag= a
XX
PN WO9613582-A1.
XX
PD 09-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US13918.
XX
PR 26-OCT-1994; 94US-0329603.
XX
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
XX
PI Dooner HK, James DW, Keller J, Lim E;
XX
DR WPI; 1996-239495/24.
DR P-PSDB; AAR95594.
XX
PT New DNA constructs contg. FAE1 gene sequences - used to produce
PT transgenic plants with modified fatty acid content in plant organs
PT or parts, esp. seeds
XX
PS Claim 3; Page 35; 48pp; English.
XX
CC A cDNA clone (AAT27036) codes for the fatty acid elongation enzyme
CC FAE1 (AAR95594) that catalyses the conversion of oleic acid (18:1) to
CC eicosenoic acid (20:1) and of eicosenoic acid to erucic acid
CC (22:1). It was isolated from a cDNA library prepd. from 2-3 wk old
CC Arabidopsis green siliques by screening with a a probe obtd. by
CC inverse PCR amplification (see also AAT27038-39) of a mutant FAE1
CC gene. The cDNA can be linked in antisense orientation to a
CC promoter, pref. a seed-specific plant promoter, and used to produce
CC transgenic plants, esp. of Brassica napus, with reduced very long
CC chain fatty acid (VLCFA) content useful for edible prodn. Sense
CC constructs provide increased VLCFA prodn. for industrial use.
XX
SQ Sequence 1641 BP; 449 A; 342 C; 355 G; 495 T; 0 other;

Query Match 44.6%; Score 652.4; DB 17; Length 1641;
Best Local Similarity 67.1%; Pred. No. 7.6e-179;
Matches 979; Conservative 0; Mismatches 436; Indels 45; Gaps 2;

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Qy        44 ACGTCAAGCTTGGTTATCACTATCTGATCACTCACTTTTTTAAACTCATGTTCCTCCCTC 103
Db        14 ACGTTAAGCTCCTTTACCGTTACGTCTTAACCAACTTTTTCAACCTCTGTTTGTTCCCGT 73

Qy       104 TAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAGCCTAAACCATCTTCAG------- 156
Db        74 TAACGGCGTTCCTCGCCGGAAAAGCCTCTCGGCTTACCATAAACGATCTCCACAACTTCC 133

Qy       157 --------CTCTATTACAATTCCACCGGATTCATCTTCGTCATTACTCTCGCCATTGTCG 208
Db       134 TTTCCTATCTCCAACACAACCTTATAACAGTAACTTTACTCTTTGCTTTCACTGTTTTCG 193

Qy       209 GATCCATTGTCTTCTTCATGTCTCGACCTAGATCCATCTACCTTCTAGATTACTCTTGCT 268
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Db        194 GTTTGGTTCTCTACATCGTAACCCGACCCAATCCGGTTTATCTCGTTGACTACTCGTGTT 253
Qy        269 ACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAAATTCATGAACAACTCTAGTTTGA 328
Db        254 ACCTTCCACCACCGCATCTCAAAGTTAGTGTCTCTAAAGTCATGGATATTTTCTACCAAA 313
Qy        329 TTCAAGATTTCAGCGAAACTTCT----------------------------CTTGAGT 358
Db        314 TAAGAAAAGCTGATACTTCTTCACGGAACGTGGCATGTGATGATCCGTCCTCGCTCGATT 373
Qy        359 TCCAGAGGAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTA 418
Db        374 TCCTGAGGAAGATTCAAGAGCGTTCAGGTCTAGGTGATGAGACGTACAGTCCTGAGGGAC 433
Qy        419 TTCACTCTATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAA 478
Db        434 TCATTCACGTACCACCGCGGAAGACTTTTGCAGCGTCACGTGAAGAGACAGAGAAGGTTA 493
Qy        479 TCTTCGGTGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTG 538
Db        494 TCATCGGTGCGCTCGAAAATCTATTCGAGAACACCAAAGTTAACCCTAGAGAGATTGGTA 553
Qy        539 TTCTTGTTGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTA 598
Db        554 TACTTGTGGTGAACTCAAGCATGTTTAATCCAACTCCTTCGCTATCCGCTATGGTCGTTA 613
Qy        599 ACAAGTATAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTG 658
Db        614 ATACTTTCAAGCTCCGAAGTAACATCAAAAGCTTTAATCTAGGAGGAATGGGTTGTAGTG 673
Qy        659 CTGGTGTTATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTG 718
Db        674 CTGGTGTTATTGCCATTGATTTGGCTAAAGACTTGTTGCATGTTCATAAAAACACTTATG 733
Qy        719 CTCTTGTGGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAA 778
Db        734 CTCTTGTGGTGAGCACTGAGAACATCACACAAGGCATTTATGCTGGAGAAAATAGATCAA 793
Qy        779 TGTTGATCCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGC 838
Db        794 TGATGGTTAGCAATTGCTTGTTTCGTGTTGGTGGGGCCGCGATTTTGCTCTCTAACAAGT 853
Qy        839 CTTTGGATCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGAT 898
Db        854 CGGGAGACCGGAGACGGTCCAAGTACAAGCTAGTTCACACGGTCCGAACGCATACTGGAG 913
Qy        899 CTGATGAGAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAG 958
Db        914 CTGATGACAAGTCTTTTCGATGTGTGCAACAAGAAGACGATGAGAGCGGCAAAATCGGAG 973
Qy        959 TTTCTTTGTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTT 1018
Db        974 TTTGTCTGTCAAAGGACATAACCAATGTTGCGGGGACAACACTTACGAAAAATATAGCAA 1033
Qy       1019 CTTTGGGTCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTG 1078
Db       1034 CATTGGGTCCGTTGATTCTTCCTTTAAGCGAAAAGTTTCTTTTTTTCGCTACCTTCGTCG 1093
Qy       1079 CTAAGAGATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTT 1138
Db       1094 CCAAGAAACTTCTAAAGGATAAAATCAAGCATTACTATGTTCCGGATTTCAAGCTTGCTG 1153
Qy       1139 TAGATCATTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTT 1198
Db       1154 TTGACCATTTCTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGAGCTAGAGAAGAACT 1213
Qy       1199 TAAAGCTTTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACA 1258
Db       1214 TAGGACTATCGCCGATCGATGTGGAGGCATCTAGATCAACGTTACATAGATTTGGGAATA 1273
Qy       1259 CTTCCTCTAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGA 1318
Db       1274 CTTCATCTAGCTCAATTTGGTATGAATTAGCATACATAGAGGCAAAGGGAAGAATGAAGA 1333
Qy       1319 AAGGAAACAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTT 1378
Db       1334 AAGGGAATAAAGCTTGGCAGATTGCTTTAGGATCAGGGTTTAAGTGTAATAGTGCGGTTT 1393
Qy       1379 GGGTGGCTCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATA 1438
Db       1394 GGGTGGCTCTACGCAATGTCAAGGCATCGGCAAATAGTCCTTGGCAACATTGCATCGATA 1453
Qy       1439 GATATCCGGTTAAGATCGAT 1458
Db       1454 GATATCCGGTTAAAATTGAT 1473
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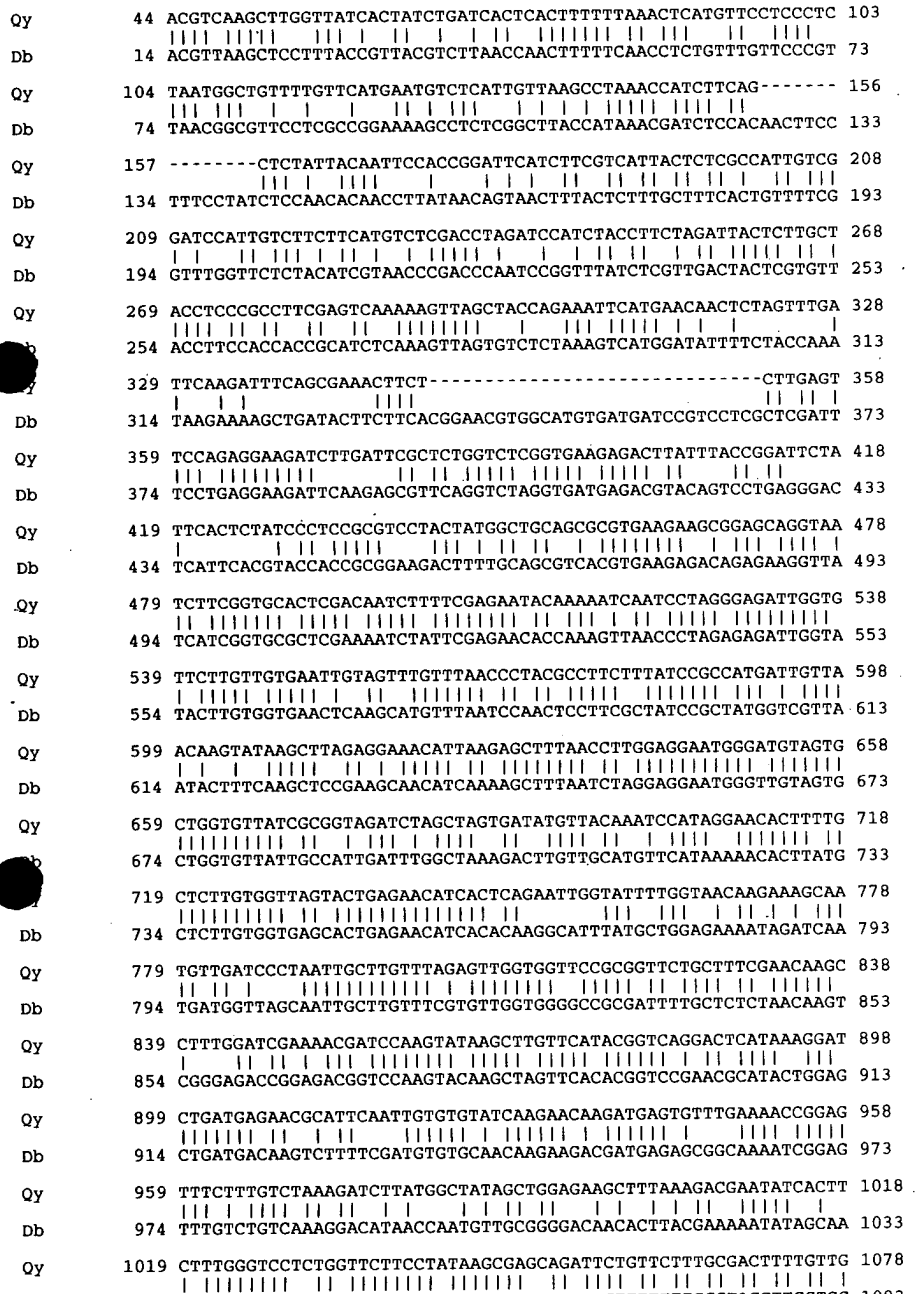
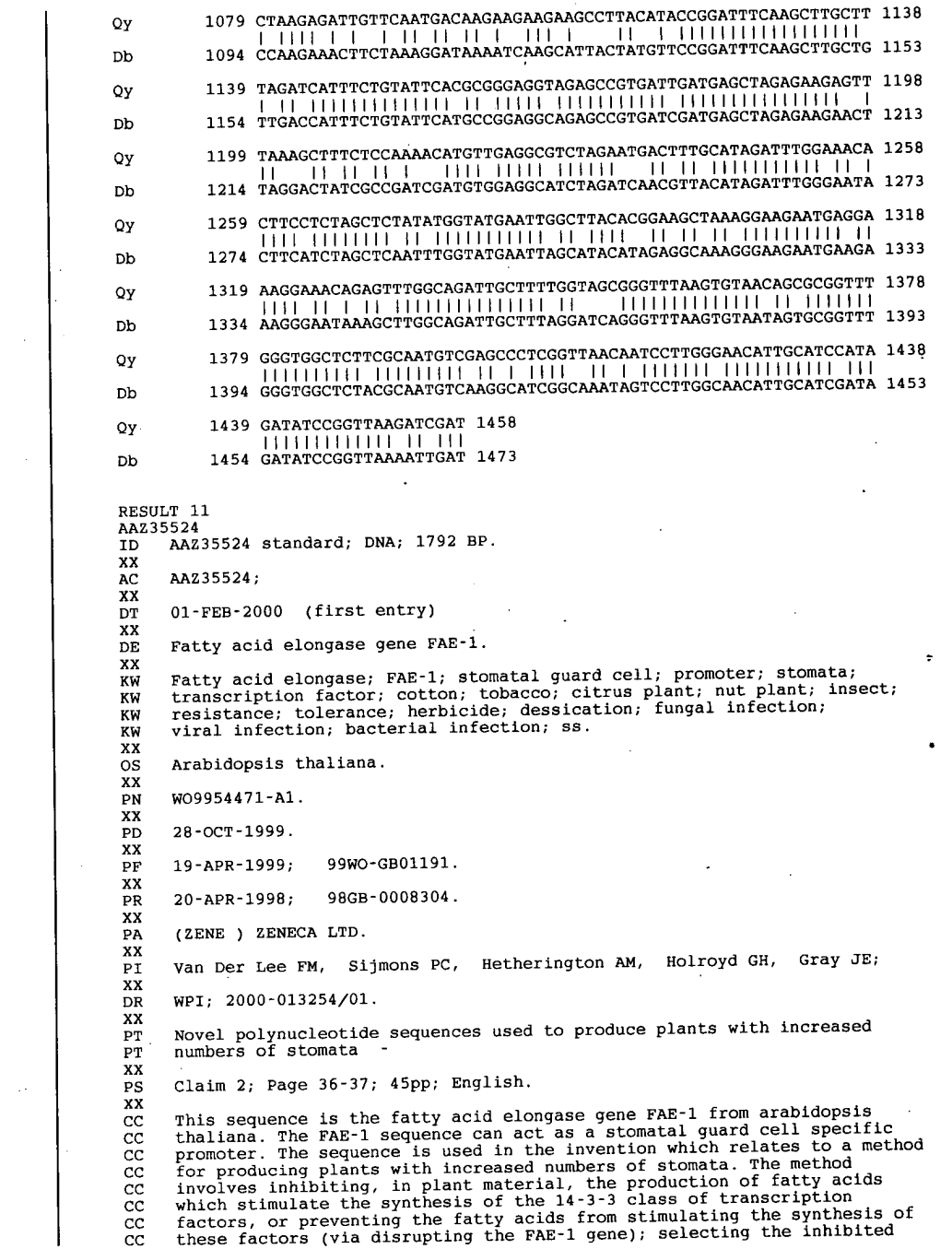
RESULT 10
AAD28500
ID AAD28500 standard; DNA; 1709 BP.
XX
AC AAD28500;
XX
DT 22-APR-2002 (first entry)
XX
DE Arabidopsis thaliana FAE1 gene.
XX
KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW very long chain fatty acid; VLCFA; FAE1 gene; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key   Location/Qualifiers
FT CDS   1..1521
FT   /*tag= a
FT   /product= "Arabidopsis thaliana FAE1 protein"
XX
PN WO200194565-A2.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US18737.
XX
PR 08-JUN-2000; 2000US-210326P.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Jaworski JG, Blacklock BJ;
XX
DR WPI; 2002-154572/20.
DR P-PSDB; AAE17608.
XX
PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
PT acids encoding the polypeptide, useful for producing very long chain
PT fatty acids
XX
PS Example 1; Fig 2-1; 139pp; English.
XX
CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
CC (KCS) polypeptides with altered substrate specificity and/or catalytic
CC activity and nucleic acid molecules encoding such polypeptides.
CC Polypeptides of the invention are useful for catalysing the condensation
CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
CC of C20 fatty acyl CoA. They are especially useful for producing very
CC long chain fatty acids (VLCFA) and may be used in the development of
CC reagents for various purposes, e.g., immunological reagents to monitor
CC expression of elongase KCS polypeptides or nucleic acid probes or
CC primers to monitor inheritance of an elongase KCS gene in plant breeding
CC programs. The present sequence is Arabidopsis thaliana FAE1 gene. This
CC gene codes for elongase KCS protein.
XX
SQ Sequence 1709 BP; 466 A; 356 C; 363 G; 524 T; 0 other;

Query Match   44.6%; Score 652.4; DB 24; Length 1709;
Best Local Similarity 67.1%; Pred. No. 7.7e-179;
Matches 979; Conservative   0; Mismatches 436; Indels   45; Gaps   2;





RESULT 11
AAZ35524
ID AAZ35524 standard; DNA; 1792 BP.
XX
AC AAZ35524;
XX
DT 01-FEB-2000 (first entry)
XX
DE Fatty acid elongase gene FAE-1.
XX
KW Fatty acid elongase; FAE-1; stomatal guard cell; promoter; stomata;
KW transcription factor; cotton; tobacco; citrus plant; nut plant; insect;
KW resistance; tolerance; herbicide; dessication; fungal infection;
KW viral infection; bacterial infection; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO9954471-A1.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-GB01191.
XX
PR 20-APR-1998; 98GB-0008304.
XX
PA (ZENE) ZENECA LTD.
XX
PI Van Der Lee FM, Sijmons PC, Hetherington AM, Holroyd GH, Gray JE;
XX
DR WPI; 2000-013254/01.
XX
PT Novel polynucleotide sequences used to produce plants with increased
PT numbers of stomata -
XX
PS Claim 2; Page 36-37; 45pp; English.
XX
CC This sequence is the fatty acid elongase gene FAE-1 from arabidopsis
CC thaliana. The FAE-1 sequence can act as a stomatal guard cell specific
CC promoter. The sequence is used in the invention which relates to a method
CC for producing plants with increased numbers of stomata. The method
CC involves inhibiting, in plant material, the production of fatty acids
CC which stimulate the synthesis of the 14-3-3 class of transcription
CC factors, or preventing the fatty acids from stimulating the synthesis of
CC these factors (via disrupting the FAE-1 gene); selecting the inhibited

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CC   material; regenerating plants from it; and selecting plants with
CC   increased numbers of stomata. The sequence can also be used to produce a
CC   vector which can be introduced into plant cells to induce greater stomata
CC   expression. The methods are used to produce plants with increased numbers
CC   of stomata on their leaves. Plants which can be used in the methods of
CC   the invention include soybean, cotton, tobacco, sugarbeet, oilseed rape,
CC   canola, flax, sunflower, potato, tomato, alfalfa, lettuce, maize, wheat,
CC   sorghum, rye, bananas, barley, oat, turf grass, forage grass, sugar cane,
CC   pea, field bean, rice, pine poplar, apple, grape, vines, cucumbers,
CC   peppers, citrus and nut plants. The plants may also be transformed with
CC   genes which provide resistance or tolerance to herbicides, insects,
CC   desiccation and/or fungal, bacterial or viral infections.
XX
SQ   Sequence 1792 BP; 501 A; 377 C; 373 G; 541 T; 0 other;

  Query Match             44.6%;  Score 652.4;  DB 21;  Length 1792;
  Best Local Similarity   67.1%;  Pred. No. 7.9e-179;
  Matches  979;  Conservative    0;  Mismatches  436;  Indels   45;  Gaps    2;

Qy         44 ACGTCAAGCTTGGTTATCACTATCTGATCACTCACTTTTTAAACTCATGTTCCTCCCTC 103
Db         97 ACGTTAAGCTCCTTTACCGTTACGTCTTAACCAACTTTTCAACCTCTGTTTGTTCCCGT 156

Qy        104 TAATGGCTGTTTGTTCATGAATGTCTCATTGTTAAGCCTAAACCATCTTCAG------- 156
Db        157 TAACGGCGTTCCTCGCCGGAAAAGCCTCTCGGCTTACCATAAACGATCTCCACAACTTCC 216

Qy        157 --------CTCTATTACAATTCCACCGGATTCATCTTCGTCATTACTCTCGCCATTGTCG 208
Db        217 TTTCCTATCTCCAACACAACCTTATAACAGTAACTTTACTCTTTGCTTTCACTGTTTTCG 276

Qy        209 GATCCATTGTCTTCTTCATGTCTCGACCTAGATCCATCTACCTTCTAGATTACTCTTGCT 268
Db        277 GTTTGGTTCTCTACATCGTAACCCGACCCAATCCGGTTTATCTCGTTGACTACTCGTGTT 336

Qy        269 ACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAAATTCATGAACAACTCTAGTTTGA 328
Db        337 ACCTTCCACCACCGCATCTCAAAGTTAGTGTCTCTAAAGTCATGGATATTTTCTACCAAA 396

Qy        329 TTCAAGATTTCAGCGAAACTTCT------------------------------CTTGAGT 358
Db        397 TAAGAAAAGCTGATACTTCTTCACGGAACGTGGCATGTGATGATCCGTCCTCGCTCGATT 456

Qy        359 TCCAGAGGAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTA 418
Db        457 TCCTGAGGAAGATTCAAGAGCGTTCAGGTCTAGGTGATGAGACGTACAGTCCTGAGGGAC 516

Qy        419 TTCACTCTATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAA 478
Db        517 TCATTCACGTACCACCGCGGAAGACTTTTGCAGCGTCACGTGAAGAGACAGAGAAGGTTA 576

Qy        479 TCTTCGGTGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTG 538
Db        577 TCATCGGTGCGCTCGAAAATCTATTCGAGAACACCAAAGTTAACCCTAGAGAGATTGGTA 636

Qy        539 TTCTTGTTGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTA 598
Db        637 TACTTGTGGTGAACTCAAGCATGTTTAATCCAACTCCTTCGCTATCCGCTATGGTCGTTA 696

Qy        599 ACAAGTATAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTG 658
Db        697 ATACTTTCAAGCTCCGAAGCAACATCAAAAGCTTTAATCTAGGAGGAATGGGTTGTAGTG 756

Qy        659 CTGGTGTTATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTG 718
Db        757 CTGGTGTTATTGCCATTGATTTGGCTAAAGACTTGTTGCATGTTCATAAAAACACTTATG 816

Qy        719 CTCTTGTGGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAA 778
Db        817 CTCTTGTGGTGAGCACTGAGAACATCACACAAGGCATTTATGCTGGAGAAAATAGATCAA 876

Qy        779 TGTTGATCCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGC 838
Db        877 TGATGGTTAGCAATTGCTTGTTTCGTGTTGGTGGGGCCGCGATTTTGCTCTCTAACAAGT 936

Qy        839 CTTTGGATCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGAT 898
Db        937 CGGGAGACCGGAGACGGTCCAAGTACAAGCTAGTTCACACGGTCCGAACGCATACTGGAG 996

Qy        899 CTGATGAGAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAG 958
Db        997 CTGATGACAAGTCTTTCGATGTGTGCAACAAGAAGACGATGAGAGCGGCAAAATCGGAG 1056

Qy        959 TTTCTTTGTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTT 1018
Db       1057 TTTGTCTGTCAAAGGACATAACCAATGTTGCGGGGACAACACTTACGAAAAATATAGCAA 1116

Qy       1019 CTTTGGGTCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTG 1078
Db       1117 CATTGGGTCCGTTGATTCTTCCTTTAAGCGAAAAGTTTCTTTTTTCGCTACCTTCGTCG 1176

Qy       1079 CTAAGAGATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTT 1138
Db       1177 CCAAGAAACTTCTAAAGGATAAAATCAAGCATTACTATGTTCCGGATTTCAAGCTTGCTG 1236

Qy       1139 TAGATCATTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTT 1198
Db       1237 TTGACCATTTCTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGAGCTAGAGAAGAACT 1296

Qy       1199 TAAAGCTTTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACA 1258
Db       1297 TAGGACTATCGCCGATCGATGTGGAGGCATCTAGATCAACGTTACATAGATTTGGGAATA 1356

Qy       1259 CTTCCTCTAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGA 1318
Db       1357 CTTCATCTAGCTCAATTTGGTATGAATTAGCATACATAGAGGCAAAGGGAAGAATGAAGA 1416

Qy       1319 AAGGAAACAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTT 1378
Db       1417 AAGGGAATAAAGCTTGGCAGATTGCTTTAGGATCAGGGTTTAAGTGTAATAGTGCGGTTT 1476

Qy       1379 GGGTGGCTCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATA 1438
Db       1477 GGGTGGCTCTACGCAATGTCAAGGCATCGGCAAATAGTCCTTGGCAACATTGCATCGATA 1536

Qy       1439 GATATCCGGTTAAGATCGAT 1458
Db       1537 GATATCCGGTTAAAATTGAT 1556

RESULT 12
AAD28517
ID   AAD28517 standard; DNA; 1709 BP.
XX
AC   AAD28517;.
XX
DT   22-APR-2002  (first entry)
XX
DE   Arabidopsis thaliana FAE1 gene mutant, At K92R.
XX
KW   Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW   very long chain fatty acid; VLCFA; FAE1 gene; mutant; ds.
XX
OS   Arabidopsis thaliana.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1521
FT                   /*tag= a
FT                   /product= "Arabidopsis thaliana FAE1 protein
FT                   mutant, At K92R"
FT   mutation        replace (275, A)
FT                   /*tag= b
XX
PN   WO200194565-A2.
XX
PD   13-DEC-2001.
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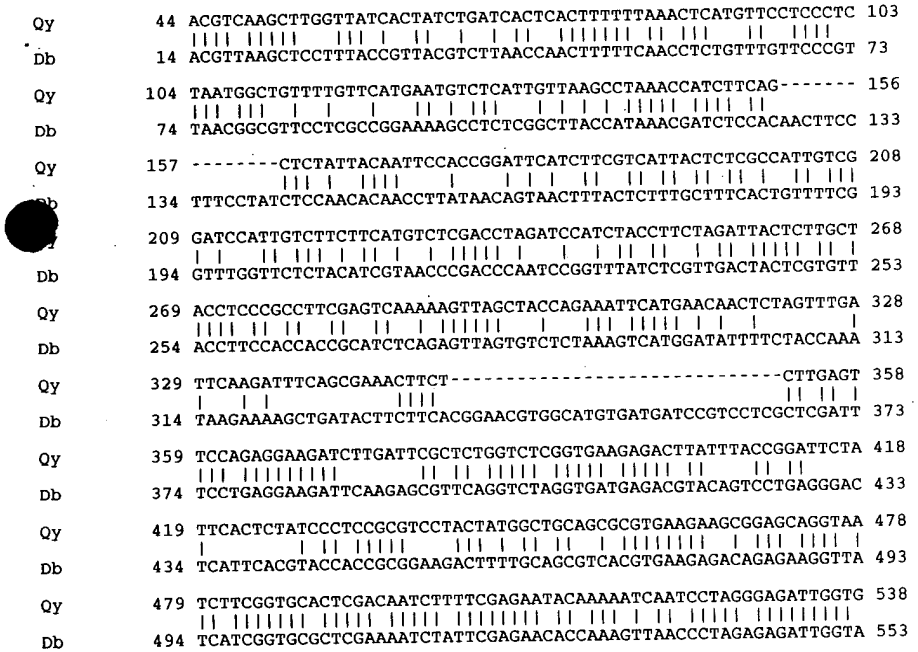
XX
PF 08-JUN-2001; 2001WO-US18737.
XX
PR 08-JUN-2000; 2000US-210326P.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Jaworski JG, Blacklock BJ;
XX
DR WPI; 2002-154572/20.
DR P-PSDB; AAE17625.
XX
PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
PT acids encoding the polypeptide, useful for producing very long chain
PT fatty acids -
XX
PS Disclosure; Fig 2-18; 139pp; English.
XX
CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
CC (KCS) polypeptides with altered substrate specificity and/or catalytic
CC activity and nucleic acid molecules encoding such polypeptides.
CC Polypeptides of the invention are useful for catalysing the condensation
CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
CC of C20 fatty acyl CoA. They are especially useful for producing very
CC long chain fatty acids (VLCFA) and may be used in the development of
CC reagents for various purposes, e.g., immunological reagents to monitor
CC expression of elongase KCS polypeptides or nucleic acid probes or
CC primers to monitor inheritance of an elongase KCS gene in plant breeding
CC programs. The present sequence is a mutant of Arabidopsis thaliana
CC elongase KCS protein encoding FAE1 gene designated as At K92R.
XX
SQ Sequence 1709 BP; 465 A; 356 C; 364 G; 524 T; 0 other;

Query Match 44.5%; Score 650.8; DB 24; Length 1709;
Best Local Similarity 67.0%; Pred. No. 2.2e-178;
Matches 978; Conservative 0; Mismatches 437; Indels 45; Gaps 2;



RESULT 13
AAD28513
ID AAD28513 standard; DNA; 1521 BP.
XX
AC AAD28513;
XX
DT 22-APR-2002 (first entry)
XX

```
DE   Brassica napus elongase KCS-A. thaliana FAE1 chimeric gene, Bn176.
XX
KW   Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW   very long chain fatty acid; VLCFA; FAE1 gene; chimeric; ds.
XX
OS   Chimeric - Brassica napus.
OS   Chimeric - Arabidopsis thaliana.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1521
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FT                   /product= "Brassica napus elongase KCS-A. thaliana FAE1
FT                   chimeric protein, Bn176"
FT   misc_feature    1..528
FT                   /*tag= b
FT                   /note= "Brassica napus elongase KCS gene"
FT   misc_feature    529..1521
FT                   /*tag= c
FT                   /note= "Arabidopsis thaliana FAE1 gene"
XX
PN   WO200194565-A2.
XX
PD   13-DEC-2001.
XX
PF   08-JUN-2001; 2001WO-US18737.
XX
PR   08-JUN-2000; 2000US-210326P.
XX
PA   (UYMI-) UNIV MIAMI.
XX
PI   Jaworski JG,  Blacklock BJ;
XX
DR   WPI; 2002-154572/20.
DR   P-PSDB; AAE17621.
XX
PT   New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
PT   acids encoding the polypeptide, useful for producing very long chain
PT   fatty acids -
XX
PS   Disclosure; Fig 2-14; 139pp; English.
XX
CC   The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
CC   (KCS) polypeptides with altered substrate specificity and/or catalytic
CC   activity and nucleic acid molecules encoding such polypeptides.
CC   Polypeptides of the invention are useful for catalysing the condensation
CC   of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
CC   of C20 fatty acyl CoA. They are especially useful for producing very
CC   long chain fatty acids (VLCFA) and may be used in the development of
CC   reagents for various purposes, e.g., immunological reagents to monitor
CC   expression of elongase KCS polypeptides or nucleic acid probes or
CC   primers to monitor inheritance of an elongase KCS gene in plant breeding
CC   programs. The present sequence is Brassica napus elongase KCS-
CC   Arabidopsis thaliana FAE1 chimeric gene designated as Bn176.
XX
SQ   Sequence 1521 BP; 421 A; 333 C; 346 G; 421 T; 0 other;

  Query Match           44.2%;  Score 647.6;  DB 24;  Length 1521;
  Best Local Similarity 66.8%;  Pred. No. 1.8e-177;
  Matches  976;  Conservative    0;  Mismatches  439;  Indels   45;  Gaps    2;

Qy        44 ACGTCAAGCTTGGTTATCACTATCTGATCACTCACTTTTTTAAACTCATGTTCCTCCCTC 103
Db        14 ACGTAAAGCTCCTTTACCATTACGTCATAACCAACCTTTTCAACCTTTGCTTCTTTCCGT 73

Qy       104 TAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAGCCTAAACCATCTTCAGCTCTATT 163
Db        74 TAACGGCGATCGTCGCCGGAAAAGCCTATCGGCTTACCATAGACGATCTTCACCACTTAT 133

Qy       164 ACAATTCCACCGGATTCATCTTCGTCATTACTCTCG----------------CCATTG 205
Db       134 ACTATTCCTATCTCCAACACAACCTCATAACCATCGCTCCACTCTTTGCCTTCACCGTTT 193

Qy       206 TCGGATCCATTGTCTTCTTCATGTCTCGACCTAGATCCATCTACCTTCTAGATTACTCTT 265

Db       194 TCGGTTCGGTTCTCTACATCGCAACCCGGCCCAAACCGGTTTACCTCGTTGAGTACTCAT 253

Qy       266 GCTACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAAATTCATGAACAACTCTAGTT 325
Db       254 GCTACCTTCCACCAACGCATTGTAGATCAAGTATCTCCAAGGTCATGGATATCTTTTATC 313

Qy       326 TGATTCAAGATTTCAGCGAAACT----------------------------TCTCTTGAGT 358
Db       314 AAGTAAGAAAAGCTGATCCTTCTCGGAACGGCACGTGCGATGACTCGTCGTGGCTTGACT 373

Qy       359 TCCAGAGGAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTA 418
Db       374 TCTTGAGGAAGATTCAAGAACGTTCAGGTCTAGGCGATGAAACTCACGGGCCCGAGGGGC 433

Qy       419 TTCACTCTATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAA 478
Db       434 TGCTTCAGGTCCCTCCCCGGAAGACTTTTGCGGCGGCGCGTGAAGAGACGGAGCAAGTTA 493

Qy       479 TCTTCGGTGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTG 538
Db       494 TCATTGGTGCGCTAGAAAATCTATTCAAGAACACCAAAGTTAACCCTAGAGAGATTGGTA 553

Qy       539 TTCTTGTTGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTA 598
Db       554 TACTTGTGGTGAACTCAAGCATGTTTAATCCAACTCCTTCGCTATCCGCTATGGTCGTTA 613

Qy       599 ACAAGTATAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTG 658
Db       614 ATACTTTCAAGCTCCGAAGCAACATCAAAAGCTTTAATCTAGGAGGAATGGGTTGTAGTG 673

Qy       659 CTGGTGTTATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTG 718
Db       674 CTGGTGTTATTGCCATTGATTTGGCTAAAGACTTGTTGCATGTTCATAAAAACACTTATG 733

Qy       719 CTCTTGTGGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAA 778
Db       734 CTCTTGTGGTGAGCACTGAGAACATCACACAAGGCATTTATGCTGGAGAAAATAGATCAA 793

Qy       779 TGTTGATCCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGC 838
Db       794 TGATGGTTAGCAATTGCTTGTTTCGTGTTGGTGGGGCCGCGATTTTGCTCTCTAACAAGT 853

Qy       839 CTTTGGATCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGAT 898
Db       854 CGGGAGACCGGAGACGGTCCAAGTACAAGCTAGTTCACACGGTCCGAACGCATACTGGAG 913

Qy       899 CTGATGAGAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAG 958
Db       914 CTGATGACAAGTCTTTTCGATGTGTGCAACAAGAAGATGATGAGAGCGGCAAAATCGGAG 973

Qy       959 TTTCTTTGTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTT 1018
Db       974 TTTGTCTGTCAAAGGACATAACCAATGTTGCGGGGACAACACTTACGAAAAATATAGCAA 1033

Qy      1019 CTTTGGGTCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTG 1078
Db      1034 CATTGGGTCCGTTGATTCTTCCTTTAAGCGAAAAGTTTCTTTTTTTCGCTACCTTCGTCG 1093

Qy      1079 CTAAGAGATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTT 1138
Db      1094 CCAAGAAACTTCTAAAGGATAAAATCAAGCATTACTATGTTCCGGATTTCAAGCTTGCTG 1153

Qy      1139 TAGATCATTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTT 1198
Db      1154 TTGACCATTTCTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGAGCTAGAGAAGAACT 1213

Qy      1199 TAAAGCTTTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACA 1258
Db      1214 TAGGACTATCGCCGATCGATGTGGAGGCATCTAGATCAACGTTACATAGATTTGGGAATA 1273

Qy      1259 CTTCCTCTAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGA 1318
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Db       1274 CTTCATCTAGCTCAATTTGGTATGAATTAGCATACATAGAGGCAAAGGGAAGAATGAAGA 1333

Qy       1319 AAGGAAACAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTT 1378

Db       1334 AAGGGAATAAAGCTTGGCAGATTGCTTTAGGATCAGGGTTTAAGTGTAATAGTGCGGTTT 1393

Qy       1379 GGGTGGCTCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATA 1438

Db       1394 GGGTGGCTCTACGCAATGTCAAGGCATCGGCAAATAGTCCTTGGCAACATTGCATCGATA 1453

Qy       1439 GATATCCGGTTAAGATCGAT 1458

Db       1454 GATATCCGGTTAAAATTGAT 1473
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RESULT 14
AAD28514
ID AAD28514 standard; DNA; 1521 BP.
XX
AC AAD28514;
XX
DT 22-APR-2002 (first entry)
XX
DE A. thaliana FAE1-Brassica napus elongase KCS chimeric gene, At399.
XX
KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW very long chain fatty acid; VLCFA; FAE1 gene; chimeric; ds.
XX
OS Chimeric - Arabidopsis thaliana.
OS Chimeric - Brassica napus.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..1521
FT		/*tag= a
FT		/product= "A. thaliana FAE1-Brassica napus elongase KCS
FT		chimeric protein, At399"
FT	misc_feature	1..1197
FT		/*tag= b
FT		/note= "Arabidopsis thaliana FAE1 gene"
FT	misc_feature	1198..1521
FT		/*tag= c
FT		/note= "Brassica napus elongase KCS gene"

XX
PN WO200194565-A2.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US18737.
XX
PR 08-JUN-2000; 2000US-210326P.
XX
PA (UYMI-) UNIV MIAMI.
XX
PI Jaworski JG, Blacklock BJ;
XX
DR WPI; 2002-154572/20.
DR P-PSDB; AAE17622.
XX
PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
PT acids encoding the polypeptide, useful for producing very long chain
PT fatty acids -
XX
PS Disclosure; Fig 2-15; 139pp; English.
XX
CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
CC (KCS) polypeptides with altered substrate specificity and/or catalytic
CC activity and nucleic acid molecules encoding such polypeptides.
CC Polypeptides of the invention are useful for catalysing the condensation
CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
CC of C20 fatty acyl CoA. They are especially useful for producing very
CC long chain fatty acids (VLCFA) and may be used in the development of
CC reagents for various purposes, e.g., immunological reagents to monitor
CC expression of elongase KCS polypeptides or nucleic acid probes or
CC primers to monitor inheritance of an elongase KCS gene in plant breeding
CC programs. The present sequence is Arabidopsis thaliana FAE1-
CC Brassica napus elongase KCS chimeric gene designated as At399.
XX
SQ Sequence 1521 BP; 424 A; 333 C; 336 G; 428 T; 0 other;

Query Match 43.8%; Score 641.2; DB 24; Length 1521;
Best Local Similarity 66.6%; Pred. No. 1.3e-175;
Matches 972; Conservative 0; Mismatches 443; Indels 45; Gaps 2;

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Qy         44 ACGTCAAGCTTGGTTATCACTATCTGATCACTCACTTTTTTAAACTCATGTTCCTCCCTC 103

Db         14 ACGTTAAGCTCCTTTACCGTTACGTCTTAACCAACTTTTTCAACCTCTGTTTGTTCCCGT 73

Qy        104 TAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAGCCTAAACCATCTTCAG------- 156

Db         74 TAACGGCGTTCCTCGCCGGAAAAGCCTCTCGGCTTACCATAAACGATCTCCACAACTTCC 133

Qy        157 --------CTCTATTACAATTCCACCGGATTCATCTTCGTCATTACTCTCGCCATTGTCG 208

Db        134 TTTCCTATCTCCAACACAACCTTATAACAGTAACTTTACTCTTTGCTTTCACTGTTTTCG 193

Qy        209 GATCCATTGTCTTCTTCATGTCTCGACCTAGATCCATCTACCTTCTAGATTACTCTTGCT 268

Db        194 GTTTGGTTCTCTACATCGTAACCCGACCCAATCCGGTTTATCTCGTTGACTACTCGTGTT 253

Qy        269 ACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAAATTCATGAACAACTCTAGTTTGA 328

Db        254 ACCTTCCACCACCGCATCTCAAAGTTAGTGTCTCTAAAGTCATGGATATTTTCTACCAAA 313

Qy        329 TTCAAGATTTCAGCGAAACTTCT----------CTTGAGT 358

Db        314 TAAGAAAAGCTGATACTTCTTCACGGAACGTGGCATGTGATGATCCGTCCTCGCTCGATT 373

Qy        359 TCCAGAGGAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTA 418

Db        374 TCCTGAGGAAGATTCAAGAGCGTTCAGGTCTAGGTGATGAGACGTACAGTCCTGAGGGAC 433

Qy        419 TTCACTCTATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAA 478

Db        434 TCATTCACGTACCACCGCGGAAGACTTTTGCAGCGTCACGTGAAGAGACAGAGAAGGTTA 493

Qy        479 TCTTCGGTGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTG 538

Db        494 TCATCGGTGCGCTCGAAAATCTATTCGAGAACACCAAAGTTAACCCTAGAGAGATTGGTA 553

Qy        539 TTCTTGTTGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTA 598

Db        554 TACTTGTGGTGAACTCAAGCATGTTTAATCCAACTCCTTCGCTATCCGCTATGGTCGTTA 613

Qy        599 ACAAGTATAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTG 658

Db        614 ATACTTTCAAGCTCCGAAGCAACATCAAAAGCTTTAATCTAGGAGGAATGGGTTGTAGTG 673

Qy        659 CTGGTGTTATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTG 718

Db        674 CTGGTGTTATTGCCATTGATTTGGCTAAAGACTTGTTGCATGTTCATAAAAACACTTATG 733

Qy        719 CTCTTGTGGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAA 778

Db        734 CTCTTGTGGTGAGCACTGAGAACATCACACAAGGCATTTATGCTGGAGAAAATAGATCAA 793

Qy        779 TGTTGATCCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGC 838

Db        794 TGATGGTTAGCAATTGCTTGTTTCGTGTTGGTGGGGCCGCGATTTTGCTCTCTAACAAGT 853

Qy        839 CTTTGGATCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGAT 898

Db        854 CGGGAGACCGGAGACGGTCCAAGTACAAGCTAGTTCACACGGTCCGAACGCATACTGGAG 913

Qy        899 CTGATGAGAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAG 958

Db        914 CTGATGACAAGTCTTTTCGATGTGTGCAACAAGAAGACGATGAGAGCGGCAAAATCGGAG 973
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Qy        959 TTTCTTTGTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTT 1018
Db        974 TTTGTCTGTCAAAGGACATAACCAATGTTGCGGGGACAACACTTACGAAAAATATAGCAA 1033

Qy       1019 CTTTGGGTCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTG 1078
Db       1034 CATTGGGTCCGTTGATTCTTCCTTTAAGCGAAAAGTTTCTTTTTTCGCTACCTTCGTCG 1093

Qy       1079 CTAAGAGATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTT 1138
Db       1094 CCAAGAAACTTCTAAAGGATAAAATCAAGCATTACTATGTTCCGGATTTCAAGCTTGCTG 1153

Qy       1139 TAGATCATTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTT 1198
Db       1154 TTGACCATTTCTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGTGCTAGAGAAGAACC 1213

Qy       1199 TAAAGCTTTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACA 1258
Db       1214 TAGCCCTAGCACCGATCGATGTAGAGGCATCAAGATCAACGTTACATAGATTTGGAAACA 1273

Qy       1259 CTTCCTCTAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGA 1318
Db       1274 CTTCATCTAGCTCAATATGGTATGAGTTGGCATACATAGAAGCAAAAGGAAGGATGAAGA 1333

Qy       1319 AAGGAAACAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTT 1378
Db       1334 AAGGTAATAAAGTTTGGCAGATTGCTTTAGGGTCAGGCTTTAAGTGTAACAGTGCAGTTT 1393

Qy       1379 GGGTGGCTCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATA 1438
Db       1394 GGGTGGCTCTAAACAATGTCAAAGCTTCGACAAATAGTCCTTGGGAACACTGCATCGACA 1453

Qy       1439 GATATCCGGTTAAGATCGAT 1458
Db       1454 GATACCCGGTCAAAATTGAT 1473
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```
RESULT 15
AAD28537
ID   AAD28537 standard; DNA; 1521 BP.
XX
AC   AAD28537;
XX
DT   22-APR-2002  (first entry)
XX
DE   Alternative version of At399 gene.
XX
KW   Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
KW   very long chain fatty acid; VLCFA; FAE1 gene; chimeric; ds.
XX
OS   Chimeric - Arabidopsis thaliana.
OS   Chimeric - Brassica napus.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "A. thaliana FAE1-Brassica napus elongase KCS
FT                   chimeric protein, At399"
FT                   /transl_except= (pos:1504..1506, aa:Xaa)
FT                   /note= "Xaa = Pro, Gln"
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FT                   /*tag= b
FT                   /note= "Arabidopsis thaliana FAE1 gene"
FT   misc_feature    1198..1521
FT                   /*tag= c
FT                   /note= "Brassica napus elongase KCS gene"
XX
PN   WO200194565-A2.
XX
PD   13-DEC-2001.
XX
PF   08-JUN-2001; 2001WO-US18737.
XX
PR   08-JUN-2000; 2000US-210326P.
XX
PA   (UYMI-) UNIV MIAMI.
XX
PI   Jaworski JG,  Blacklock BJ;
XX
DR   WPI; 2002-154572/20.
DR   P-PSDB; AAE17850.
XX
PT   New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
PT   acids encoding the polypeptide, useful for producing very long chain
PT   fatty acids  -
XX
PS   Disclosure; Page 111-113; 139pp; English.
XX
CC   The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
CC   (KCS) polypeptides with altered substrate specificity and/or catalytic
CC   activity and nucleic acid molecules encoding such polypeptides.
CC   Polypeptides of the invention are useful for catalysing the condensation
CC   of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
CC   of C20 fatty acyl CoA. They are especially useful for producing very
CC   long chain fatty acids (VLCFA) and may be used in the development of
CC   reagents for various purposes, e.g., immunological reagents to monitor
CC   expression of elongase KCS polypeptides or nucleic acid probes or
CC   primers to monitor inheritance of an elongase KCS gene in plant breeding
CC   programs. The present sequence is an alternative version of
CC   Arabidopsis thaliana FAE1-Brassica napus elongase KCS chimeric gene
CC   designated as At399.
XX
SQ   Sequence 1521 BP; 423 A; 333 C; 336 G; 428 T; 1 other;

  Query Match             43.8%;  Score 641.2;  DB 24;  Length 1521;
  Best Local Similarity   66.6%;  Pred. No. 1.3e-175;
  Matches  972;  Conservative    0;  Mismatches  443;  Indels   45;  Gaps    2;
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Qy         44 ACGTCAAGCTTGGTTATCACTATCTGATCACTCACTTTTTAAACTCATGTTCCTCCCTC 103
Db         14 ACGTTAAGCTCCTTTACCGTTACGTCTTAACCAACTTTTCAACCTCTGTTTGTTCCCGT 73

Qy        104 TAATGGCTGTTTTGTTCATGAATGTCTCATTGTTAAGCCTAAACCATCTTCAG------- 156
Db         74 TAACGGCGTTCCTCGCCGGAAAAGCCTCTCGGCTTACCATAAACGATCTCCACAACTTCC 133

Qy        157 --------CTCTATTACAATTCCACCGGATTCATCTTCGTCATTACTCTCGCCATTGTCG 208
Db        134 TTTCCTATCTCCAACACAACCTTATAACAGTAACTTTACTCTTTGCTTTCACTGTTTCG 193

Qy        209 GATCCATTGTCTTCTTCATGTCTCGACCTAGATCCATCTACCTTCTAGATTACTCTTGCT 268
Db        194 GTTTGGTTCTCTACATCGTAACCCGACCCAATCCGGTTTATCTCGTTGACTACTCGTGTT 253

Qy        269 ACCTCCCGCCTTCGAGTCAAAAAGTTAGCTACCAGAAATTCATGAACAACTCTAGTTTGA 328
Db        254 ACCTTCCACCACCGCATCTCAAAGTTAGTGTCTCTAAAGTCATGGATATTTTCTACCAAA 313

Qy        329 TTCAAGATTTCAGCGAAACTTCT----------------------------CTTGAGT 358
Db        314 TAAGAAAAGCTGATACTTCTTCACGGAACGTGGCATGTGATGATCCGTCCTCGCTCGATT 373

Qy        359 TCCAGAGGAAGATCTTGATTCGCTCTGGTCTCGGTGAAGAGACTTATTTACCGGATTCTA 418
Db        374 TCCTGAGGAAGATTCAAGAGCGTTCAGGTCTAGGTGATGAGACGTACAGTCCTGAGGGAC 433

Qy        419 TTCACTCTATCCCTCCGCGTCCTACTATGGCTGCAGCGCGTGAAGAAGCGGAGCAGGTAA 478
Db        434 TCATTCACGTACCACCGCGGAAGACTTTTGCAGCGTCACGTGAAGAGACAGAGAAGGTTA 493

Qy        479 TCTTCGGTGCACTCGACAATCTTTTCGAGAATACAAAAATCAATCCTAGGGAGATTGGTG 538
Db        494 TCATCGGTGCGCTCGAAAATCTATTCGAGAACACCAAAGTTAACCCTAGAGAGATTGGTA 553

Qy        539 TTCTTGTTGTGAATTGTAGTTTGTTTAACCCTACGCCTTCTTTATCCGCCATGATTGTTA 598
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Db        554 TACTTGTGGTGAACTCAAGCATGTTTAATCCAACTCCTTCGCTATCCGCTATGGTCGTTA 613

Qy        599 ACAAGTATAAGCTTAGAGGAAACATTAAGAGCTTTAACCTTGGAGGAATGGGATGTAGTG 658

Db        614 ATACTTTCAAGCTCCGAAGCAACATCAAAAGCTTTAATCTAGGAGGAATGGGTTGTAGTG 673

Qy        659 CTGGTGTTATCGCGGTAGATCTAGCTAGTGATATGTTACAAATCCATAGGAACACTTTTG 718

Db        674 CTGGTGTTATTGCCATTGATTTGGCTAAAGACTTGTTGCATGTTCATAAAAACACTTATG 733

Qy        719 CTCTTGTGGTTAGTACTGAGAACATCACTCAGAATTGGTATTTTGGTAACAAGAAAGCAA 778

Db        734 CTCTTGTGGTGAGCACTGAGAACATCACACAAGGCATTTATGCTGGAGAAAATAGATCAA 793

Qy        779 TGTTGATCCCTAATTGCTTGTTTAGAGTTGGTGGTTCCGCGGTTCTGCTTTCGAACAAGC 838

Db        794 TGATGGTTAGCAATTGCTTGTTTCGTGTTGGTGGGGCCGCGATTTTGCTCTCTAACAAGT 853

          839 CTTTGGATCGAAAACGATCCAAGTATAAGCTTGTTCATACGGTCAGGACTCATAAAGGAT 898

          854 CGGGAGACCGGAGACGGTCCAAGTACAAGCTAGTTCACACGGTCCGAACGCATACTGGAG 913

Qy        899 CTGATGAGAACGCATTCAATTGTGTGTATCAAGAACAAGATGAGTGTTTGAAAACCGGAG 958

Db        914 CTGATGACAAGTCTTTTCGATGTGTGCAACAAGAAGACGATGAGAGCGGCAAAATCGGAG 973

Qy        959 TTTCTTTGTCTAAAGATCTTATGGCTATAGCTGGAGAAGCTTTAAAGACGAATATCACTT 1018

Db        974 TTTGTCTGTCAAAGGACATAACCAATGTTGCGGGGACAACACTTACGAAAAATATAGCAA 1033

Qy       1019 CTTTGGGTCCTCTGGTTCTTCCTATAAGCGAGCAGATTCTGTTCTTTGCGACTTTTGTTG 1078

Db       1034 CATTGGGTCCGTTGATTCTTCCTTTAAGCGAAAAGTTTCTTTTTTTCGCTACCTTCGTCG 1093

Qy       1079 CTAAGAGATTGTTCAATGACAAGAAGAAGAAGCCTTACATACCGGATTTCAAGCTTGCTT 1138

Db       1094 CCAAGAAACTTCTAAAGGATAAAATCAAGCATTACTATGTTCCGGATTTCAAGCTTGCTG 1153

Qy       1139 TAGATCATTTCTGTATTCACGCGGGAGGTAGAGCCGTGATTGATGAGCTAGAGAAGAGTT 1198

Db       1154 TTGACCATTTCTGTATTCATGCCGGAGGCAGAGCCGTGATCGATGTGCTAGAGAAGAACC 1213

Qy       1199 TAAAGCTTTCTCCAAAACATGTTGAGGCGTCTAGAATGACTTTGCATAGATTTGGAAACA 1258

Db       1214 TAGCCCTAGCACCGATCGATGTAGAGGCATCAAGATCAACGTTACATAGATTTGGAAACA 1273

         1259 CTTCCTCTAGCTCTATATGGTATGAATTGGCTTACACGGAAGCTAAAGGAAGAATGAGGA 1318

         1274 CTTCATCTAGCTCAATATGGTATGAGTTGGCATACATAGAAGCAAAAGGAAGGATGAAGA 1333

Qy       1319 AAGGAAACAGAGTTTGGCAGATTGCTTTTGGTAGCGGGTTTAAGTGTAACAGCGCGGTTT 1378

Db       1334 AAGGTAATAAAGTTTGGCAGATTGCTTTAGGGTCAGGCTTTAAGTGTAACAGTGCAGTTT 1393

Qy       1379 GGGTGGCTCTTCGCAATGTCGAGCCCTCGGTTAACAATCCTTGGGAACATTGCATCCATA 1438

Db       1394 GGGTGGCTCTAAACAATGTCAAAGCTTCGACAAATAGTCCTTGGGAACACTGCATCGACA 1453

Qy       1439 GATATCCGGTTAAGATCGAT 1458

Db       1454 GATACCCGGTCAAAATTGAT 1473

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Job time : 370 secs
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